SEQUENCE LISTING

<110> Kilian, Andrzej
Bowtell, David

<120> VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES THEREOF

<130> 082447-0104

<140> 09/502,424
<141> 2000-02-11

<160> 155

<170> PatentIn Ver. 2.0

<210> 1
<211> 3964
<212> DNA
<213> Homo sapiens

<400> 1
atgccgcgcg ctccccgctg ccgagccgtg cgctcccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcgggggga gcggggcgtg ggggctgctg 420
ttgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
ctgtggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
ctgcggccct gcagcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1140
gtggagacca tcttttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1200
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcggggctg cgcttggctg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100

gacccgccgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacaccatc 2160
ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccccagaa cacgtactgc 2220
gtgcgtcggt atgccgtggt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280
agccacgtct ctaccttgac agacctccag ccgtacatgc gacagttcgt ggctcacctg 2340
caggagacca gcccgctgag ggatgccgtc gtcatcgagc agagctcctc cctgaatgag 2400
gccagcagtg gcctcttcga cgtcttccta cgcttcatgt gccaccacgc cgtgcgcatc 2460
aggggcaagt cctacgtcca gtgccagggg atcccgcagg gctccatcct ctccacgctg 2520
ctctgcagcc tgtgctacgg cgacatggag aacaagctgt ttgcggggat tcggcgggac 2580
gggctgctcc tgcgtttggt ggatgatttc ttgttggtga cacctcacct cacccacgcg 2640
aaaaccttcc tcaggaccct ggtccgaggt gtccctgagt atggctgcgt ggtgaacttg 2700
cggaagacag tggtgaactt ccctgtagaa gacgaggccc tgggtggcac ggcttttgtt 2760
cagatgccgg cccacggcct attcccctgg tgcggcctgc tgctggatac ccggaccctg 2820
gaggtgcaga gcgactactc cagctatgcc cggacctcca tcagagccag tctcaccttc 2880
aaccgcggct tcaaggctgg gaggaacatg cgtcgcaaac tctttggggt cttgcggctg 2940
aagtgtcaca gcctgtttct ggatttgcag gtgaacagcc tccagacggt gtgcaccaac 3000
atctacaaga tcctcctgct gcaggcgtac aggtttcacg catgtgtgct gcagctccca 3060
tttcatcagc aagtttggaa gaaccccaca tttttcctgc gcgtcatctc tgacacggcc 3120
tccctctgct actccatcct gaaagccaag aacgcaggga tgtcgctggg ggccaagggc 3180
gccgccggcc ctctgccctc cgaggccgtg cagtggctgt gccaccaagc attcctgctc 3240
aagctgactc gacaccgtgt cacctacgtg ccactcctgg ggtcactcag gacagcccag 3300
acgcagctga gtcggaagct cccggggacg acgctgactg ccctggaggc cgcagccaac 3360
ccggcactgc cctcagactt caagaccatc ctggactgat ggccacccgc ccacagccag 3420
gccgagagca gacaccagca gccctgtcac gccgggctct acgtcccagg gagggagggg 3480
cggcccacac ccaggcccgc accgctggga gtctgaggcc tgagtgagtg tttggccgag 3540
gcctgcatgt ccggctgaag gctgagtgtc cggctgaggc ctgagcgagt gtccagccaa 3600
gggctgagtg tccagcacac ctgccgtctt cacttcccca caggctggcg ctcggctcca 3660
ccccagggcc agcttttcct caccaggagc ccggcttcca ctccccacat aggaatagtc 3720
catccccaga ttcgccattg ttcacccctc gccctgccct cctttgcctt ccacccccac 3780
catccaggtg gagaccctga gaaggaccct gggagctctg ggaatttgga gtgaccaaag 3840
gtgtgccctg tacacaggcg aggaccctgc acctggatgg gggtccctgt gggtcaaatt 3900
gggggaggt gctgtgggag taaaatactg aatatatgag tttttcagtt ttgaaaaaaa 3960
aaaa 3964

<210> 2
<211> 1132
<212> PRT
<213> Homo sapiens

<400> 2
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro

```
                100                 105                 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
        115                 120                 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
    130                 135                 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145                 150                 155                 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
                165                 170                 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
            180                 185                 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
        195                 200                 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
    210                 215                 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225                 230                 235                 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
                245                 250                 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
            260                 265                 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
        275                 280                 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
    290                 295                 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305                 310                 315                 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
                325                 330                 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
            340                 345                 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
        355                 360                 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
    370                 375                 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385                 390                 395                 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
                405                 410                 415
```

D10

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540

D10

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
835 840 845

D12 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala

1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
1045 1050 1055

Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
1060 1065 1070

Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
1075 1080 1085

Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1125 1130

<210> 3
<211> 1031
<212> PRT
<213> Euplotes aediculatus

D10

<400> 3
Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
1 5 10 15

Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
20 25 30

Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
35 40 45

Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
50 55 60

Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
65 70 75 80

Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
85 90 95

Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
100 105 110

Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
115 120 125

Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
130 135 140

Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
145 150 155 160

Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln

165 170 175

Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
180 185 190

Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
195 200 205

Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
210 215 220

Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
225 230 235 240

Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
245 250 255

His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
260 265 270

Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
275 280 285

D10

Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
290 295 300

Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
305 310 315 320

Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
325 330 335

Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
340 345 350

Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
355 360 365

Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
370 375 380

Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
385 390 395 400

Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
405 410 415

Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
420 425 430

Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
435 440 445

Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
450 455 460

Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
465 470 475 480

Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
485 490 495

Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
500 505 510

Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
515 520 525

Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
530 535 540

Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
545 550 555 560

Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
565 570 575

Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
580 585 590

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
595 600 605

D10

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
610 615 620

Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
625 630 635 640

Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
645 650 655

Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly
660 665 670

Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
675 680 685

Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
690 695 700

Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
705 710 715 720

Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
725 730 735

Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
740 745 750

Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
755 760 765

Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
770 775 780

Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
785 790 795 800

Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
805 810 815

Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met
820 825 830

Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile
835 840 845

Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn
850 855 860

Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr
865 870 875 880

Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met
885 890 895

Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe
900 905 910

D18

Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr
915 920 925

Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala
930 935 940

Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val
945 950 955 960

Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile
965 970 975

Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His
980 985 990

Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
995 1000 1005

Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln
1010 1015 1020

Ser Leu Ile Gln Tyr Asp Ala
1025 1030

<210> 4
<211> 1104
<212> PRT
<213> Saccharomyces cerevisiae

<400> 4
Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro
1 5 10 15

Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp
20 25 30

Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys
35 40 45

Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly
50 55 60

Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg
65 70 75 80

Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro
85 90 95

Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu
100 105 110

Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys
115 120 125

Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly
130 135 140

Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro
145 150 155 160

D10

His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn
165 170 175

His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly
180 185 190

Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys
195 200 205

Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly
210 215 220

Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg
225 230 235 240

Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser
245 250 255

Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly
260 265 270

Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro
275 280 285

Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu
290 295 300

Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser
305 310 315 320

Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile

325 330 335

Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro
340 345 350

Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu
355 360 365

Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His
370 375 380

Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg
385 390 395 400

Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp
405 410 415

Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln
420 425 430

Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly
435 440 445

Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys
450 455 460

D10

Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu
465 470 475 480

Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro
485 490 495

Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile
500 505 510

Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu
515 520 525

Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg
530 535 540

Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
545 550 555 560

Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala
565 570 575

Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
580 585 590

Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
595 600 605

Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
610 615 620

Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
625 630 635 640

Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp
645 650 655

Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln
660 665 670

Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala
675 680 685

Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
690 695 700

Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
705 710 715 720

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
725 730 735

Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
740 745 750

Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
755 760 765

D10

Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
770 775 780

Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
785 790 795 800

Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
805 810 815

Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
820 825 830

Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
835 840 845

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
850 855 860

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
865 870 875 880

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
885 890 895

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
900 905 910

Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
915 920 925

Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
930 935 940

```
Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
945                 950                 955                 960

Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
                965                 970                 975

Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
            980                 985                 990

Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
        995                1000                1005

Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
   1010                1015                1020

Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
1025                1030                1035                1040

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
               1045                1050                1055

His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
           1060                1065                1070

Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
       1075                1080                1085

Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
   1090                1095                1100
```

D10

```
<210> 5
<211> 884
<212> PRT
<213> Homo sapiens

<400> 5
Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
  1               5                  10                  15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn
            20                  25                  30

Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
        35                  40                  45

Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
    50                  55                  60

Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
65                  70                  75                  80

Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
                85                  90                  95
```

Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
100 105 110

Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
115 120 125

Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
130 135 140

Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
145 150 155 160

Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
165 170 175

Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
180 185 190

Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
195 200 205

Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
210 215 220

D10 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr
225 230 235 240

Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
245 250 255

Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
260 265 270

His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
275 280 285

Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
290 295 300

Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Leu Ser Leu Pro
305 310 315 320

Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu
325 330 335

Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His
340 345 350

Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu
355 360 365

Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr
370 375 380

Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp
385 390 395 400

Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu

405 410 415

Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn
420 425 430

Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu
435 440 445

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
450 455 460

Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
465 470 475 480

Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
485 490 495

Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg
500 505 510

Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys
515 520 525

Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met
530 535 540

D10

Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
545 550 555 560

Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
565 570 575

Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
580 585 590

Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
595 600 605

Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
610 615 620

Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile
625 630 635 640

Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
645 650 655

Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
660 665 670

Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
675 680 685

Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
690 695 700

Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe
705 710 715 720

```
Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
                725                 730                 735

Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
            740                 745                 750

Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
        755                 760                 765

Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
    770                 775                 780

His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
785                 790                 795                 800

Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
                805                 810                 815

Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
            820                 825                 830

Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
        835                 840                 845

Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
    850                 855                 860

Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
865                 870                 875                 880

His Ile Val Asn
```

D10

<210> 6
<211> 13
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (8)..(13)
<223> First six bases of Y intron

<400> 6
ccaggtgggc ctc 13

<210> 7
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (1)..(7)
<223> Last seven bases of intron Y

<400> 7
gcaggtgtcc tgcc 14

<210> 8
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (8)..(14)
<223> First 7 bases of Intron 1

<400> 8
aaagagggtg gctg 14

<210> 9
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (1)..(7)
<223> Last 7 bases of Intron 1

P10

<400> 9
aacagaagcc gagc 14

<210> 10
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (8)..(14)
<223> First 7 bases of Intron Alpha

<400> 10
tgtcaaggtg gatg 14

<210> 11
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (1)..(7)
<223> Last 7 bases of Intron Alpha

<400> 11
cccccaggac aggc 14

<210> 12
<211> 14
<212> DNA

<213> Homo sapiens

<220>
<221> intron
<222> (8)..(14)
<223> First 7 bases of Intron Beta

<400> 12
gagccacgtc tcta 14

<210> 13
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (1)..(7)
<223> Last 7 bases of Intron Beta

<400> 13
ggggcaagtc ctac 14

<210> 14
<211> 14
<212> DNA
D10
<213> Homo sapiens

<220>
<221> intron
<222> (8)..(14)
<223> First 7 base of Intron 2

<400> 14
actccaggtg agcg 14

<210> 15
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1)..(7)
<223> Wherein N is any nucleotide

<220>
<221> intron
<222> (1)..(7)
<223> Last 7 bases of Intron 2

<400> 15
nnnnnnncta tgcc 14

<210> 16
<211> 173
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (8)..(166)
<223> Full Sequence of Intron 3

<400> 16
aacgcagccg aagaaaacat ttctgtcgtg actcctgcgg tgcttgggtc gggacagcca 60
gagatggagc caccccgcag accgtcgggt gtgggcagct ttccggtgtc tcctgggagg 120
ggagttgggc tgggcctgtg actcctcagc ctctgttttc ccccagggat gtc 173

<210> 17
<211> 46
<212> PRT
<213> Homo sapiens

<400> 17
Thr Ala Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
1 5 10 15

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
20 25 30

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
35 40 45

P10

<210> 18
<211> 104
<212> DNA
<213> Homo sapiens

<220>
<223> Intron Y

<400> 18
ggcctccccg gggtcggcgt ccggctgggg ttgagggcgg ccgggggggaa ccagcgacat 60
gcggagagca gcgcaggcga ctcagggcgc ttcccccgca ggtg 104

<210> 19
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<223> Reding Frame One of Intron Y

<400> 19
Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly
1 5 10 15

Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro
20 25 30

Arg Arg

<210> 20
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<223> Reading Frame Two of Intron Y before termination Codon

<400> 20
Ala Ser Pro Gly Ser Ala Ser Gly Trp Gly
1 5 10

<210> 21
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<223> Reading Frame Two of Intron Y after termination Codon

D10

<400> 21
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly
20

<210> 22
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<223> Reading Frame Three of Intron Y

<400> 22
Pro Pro Arg Gly Arg Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu
1 5 10 15

Pro Ala Thr Cys Gly Glu Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro
20 25 30

Gln Val

<210> 23
<211> 38
<212> DNA
<213> Homo sapiens

<220>
<223> Intron 1

<400> 23
gtggctgtgc tttggtttaa cttccttttt aaccagaa 38

<210> 24
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<223> Intron 1 Translation

<400> 24
Val Ala Val Leu Trp Phe Asn Phe Leu Phe Asn Gln Lys
1 5 10

<210> 25
<211> 36
<212> DNA
<213> Homo sapiens

<220>
<223> Intron Alpha

D10

<400> 25
gtggatgtga cgggcgcgta cgacaccatc ccccag 36

<210> 26
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<223> Intron Alpha Translation

<400> 26
Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln
1 5 10

<210> 27
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<223> Intron Beta

<400> 27
gtctctacct tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag 60
accagcccgc tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc 120
agtggcctct tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc 180
aa 182

<210> 28
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<223> Intron Beta Translation

<400> 28
Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
1 5 10 15

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
20 25 30

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
35 40 45

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
50 55 60

<210> 29
<211> 226
<212> DNA
<213> Homo sapiens

D10
<220>
<223> Intron 2

<400> 29
gtgagcgcac ctggccggaa gtggagcctg tgcccggctg gggcaggtgc tgctgcaggg 60
ccgttgcgtc cacctctgct tccgtgtggg gcaggcgact gccaatccca aagggtcaga 120
tgccacaggg tgcccctcgt cccatctggg gctgagcaca aatgcatctt tctgtgggag 180
tgagggtgcc tcacaacggg agcagttttc tgtgctattt tggtaa 226

<210> 30
<211> 159
<212> DNA
<213> Homo sapiens

<220>
<223> Intron 3

<400> 30
ccgaagaaaa catttctgtc gtgactcctg cggtgcttgg gtcgggacag ccagagatgg 60
agccaccccg cagaccgtcg ggtgtgggca gctttccggt gtctcctggg aggggagttg 120
ggctgggcct gtgactcctc agcctctgtt ttcccccag 159

<210> 31
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<223> Intron 3 Translation

<400> 31
Ala Glu Glu Asn Ile Ser Val Val Thr Pro Ala Val Leu Gly Ser Gly
1 5 10 15

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe

20 25 30

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
35 40

<210> 32
<211> 262
<212> DNA
<213> Homo sapiens

<220>
<223> Intron X. Complete length unknown

<400> 32
gacagtcacc agggggttg accgccggac tgggcgtccc cagggttgac tataggacca 60
ggtgtccagg tgccctgcaa gtagaggggc tctcagaggc gtctggctgg catgggtgga 120
cgtggccccg ggcatggcct tctgcgtgtg ctgccgtggg tgccctgagc cctcactgag 180
tcggtggggg cttgtggctt cccgtgagct tccccctagt ctgttgtctg gctgagcaag 240
cctcctgagg ggctctctat tg 262

<210> 33
<211> 218
<212> DNA
<213> Homo sapiens

D10

<220>
<223> Partial Sequence of Genomic Intron (approximately 2.7 kb)

<400> 33
gtggctgtgc tttggtttaa cttccttttt aaccagaagt gcgtttgagc cccacatttg 60
gtatcagctt agatgaaggg cccggaggag gggccacggg acacagccag ggccatggca 120
cggcgcccac ccatttgtgc gcacagtgag gtggccgagg tgccggtgcc tccagaaaag 180
cagcgtgggg gtgtaggggg agctcctggg gcagggac 218

<210> 34
<211> 2031
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1767)..(1769)
<223> Wherein N is A, C, G or T

<220>
<223> N-Terminal Truncated Telomerase

<400> 34
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcgggggа gcggggcgtg ggggctgctg 420
ctgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480

```
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggctg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaatnnng acagtcacca gggggggttga ccgccggact 1800
gggcgtcccc agggttgact ataggaccag gtgtccaggt gccctgcaag tagaggggct 1860
ctcagaggcg tctggctggc atgggtggac gtggccccgg gcatggcctt ctgcgtgtgc 1920
tgccgtgggt gccctgagcc ctcactgagt cggtgggggc ttgtggcttc ccgtgagctt 1980
ccccctagtc tgttgtctgg ctgagcaagc ctcctgaggg gctctctatt g           2031
```

D10

<210> 35
<211> 588
<212> PRT
<213> Homo sapiens

<220>
<223> Protein Predicted by SEQ ID NO:34

<400> 35

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
             20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
         35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65                  70                  75                  80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
                 85                  90                  95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
            100                 105                 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
```

115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

D10 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

D10

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
580 585

<210> 36
<211> 2041
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein 1; Intron 1 Addition

<400> 36
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcgggggga gcggggcgtg ggggctgctg 420
ctgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020

```
ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggctg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
ggagccagaa cgttccgcag agaaaagagg gtggctgtgc tttggtttaa cttccttttt 1980
aaccagaagc cgagcgtctc acctcgaggg tgaaggcact gttcagcgtg ctcaactacg 2040
a                                                                  2041
```

<210> 37
<211> 670
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 1; Encoded by SEQ ID NO:36

D10

<400> 37

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
            20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
        35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
    50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65                  70                  75                  80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
                85                  90                  95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
            100                 105                 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
        115                 120                 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
    130                 135                 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145                 150                 155                 160
```

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

D10

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser

```
465                 470                 475                 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
                485                 490                 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
            500                 505                 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
        515                 520                 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
    530                 535                 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545                 550                 555                 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
                565                 570                 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
            580                 585                 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
        595                 600                 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
    610                 615                 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625                 630                 635                 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe
                645                 650                 655

Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
            660                 665                 670
```

P10

<210> 38
<211> 2541
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein 2; Alpha Intron Addition

<400> 38
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420
ctgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600

cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggctg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
gacccgccgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacaccatc 2160
ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccccagaa cacgtactgc 2220
gtgcgtcggt atgccgtggt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280
agccacgtcc tacgtccagt gccaggggat cccgcagggc tccatcctct ccacgctgct 2340
ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc ggcgggacgg 2400
gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca cccacgcgaa 2460
aaccttcctc aggaccctgg tccgaggtgt ccctgagtat ggctgcgtgg tgaacttgcg 2520
gaagacagtg gtgaacttcc c 2541

D10

<210> 39
<211> 807
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 2; Encoded by SEQ ID NO:38

<400> 39
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

D10

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His

385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

D10

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
690 695 700

```
Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
705                 710                 715                 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
                725                 730                 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
            740                 745                 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro
        755                 760                 765

Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val
    770                 775                 780

Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg
785                 790                 795                 800

Ala Ala Pro Ala Phe Val Gly
                805
```

D10

<210> 40
<211> 3396
<212> DNA
<213> Homo sapiens

<220>
<223> Reference Telomerase; with Intron Alpha and Beta

<400> 40
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcgggga gcggggcgtg ggggctgctg 420
ttgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcggggctg cgcttggctg 1560

cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
gacccgccgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacaccatc 2160
ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccccagaa cacgtactgc 2220
gtgcgtcggt atgccgtggt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280
agccacgtct ctaccttgac agacctccag ccgtacatgc gacagttcgt ggctcacctg 2340
caggagacca gcccgctgag ggatgccgtc gtcatcgagc agagctcctc cctgaatgag 2400
gccagcagtg gcctcttcga cgtcttccta cgcttcatgt gccaccacgc cgtgcgcatc 2460
aggggcaagt cctacgtcca gtgccagggg atcccgcagg gctccatcct ctccacgctg 2520
ctctgcagcc tgtgctacgg cgacatggag aacaagctgt ttgcggggat tcggcgggac 2580
gggctgctcc tgcgtttggt ggatgatttc ttgttggtga cacctcacct cacccacgcg 2640
aaaaccttcc tcaggaccct ggtccgaggt gtccctgagt atggctgcgt ggtgaacttg 2700
cggaagacag tggtgaactt ccctgtagaa gacgaggccc tgggtggcac ggcttttgtt 2760
cagatgccgg cccacggcct attcccctgg tgcggcctgc tgctggatac ccggaccctg 2820
gaggtgcaga gcgactactc cagctatgcc cggacctcca tcagagccag tctcaccttc 2880
aaccgcggct tcaaggctgg gaggaacatg cgtcgcaaac tctttggggt cttgcggctg 2940
aagtgtcaca gcctgtttct ggatttgcag gtgaacagcc tccagacggt gtgcaccaac 3000
atctacaaga tcctcctgct gcaggcgtac aggtttcacg catgtgtgct gcagctccca 3060
tttcatcagc aagtttggaa gaaccccaca tttttcctgc gcgtcatctc tgacacggcc 3120
tccctctgct actccatcct gaaagccaag aacgcaggga tgtcgctggg ggccaagggc 3180
gccgccggcc ctctgccctc cgaggccgtg cagtggctgt gccaccaagc attcctgctc 3240
aagctgactc gacaccgtgt cacctacgtg ccactcctgg ggtcactcag gacagcccag 3300
acgcagctga gtcggaagct cccggggacg acgctgactg ccctggaggc cgcagccaac 3360
ccggcactgc cctcagactt caagaccatc ctggac 3396

<210> 41
<211> 3069
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein 3; with Introns Alpha, Beta and 2

<400> 41
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420
ctgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960

```
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggctg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
gacccgccgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacaccatc 2160
ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccccagaa cacgtactgc 2220
gtgcgtcggt atgccgtggt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280
agccacgtct ctaccttgac agacctccag ccgtacatgc gacagttcgt ggctcacctg 2340
caggagacca gcccgctgag ggatgccgtc gtcatcgagc agagctcctc cctgaatgag 2400
gccagcagtg gcctcttcga cgtcttccta cgcttcatgt gccaccacgc cgtgcgcatc 2460
aggggcaagt cctacgtcca gtgccagggg atcccgcagg gctccatcct ctccacgctg 2520
ctctgcagcc tgtgctacgg cgacatggag aacaagctgt ttgcggggat tcggcgggac 2580
gggctgctcc tgcgtttggt ggatgatttc ttgttggtga cacctcacct cacccacgcg 2640
aaaaccttcc tcaggaccct ggtccgaggt gtccctgagt atggctgcgt ggtgaacttg 2700
cggaagacag tggtgaactt ccctgtagaa gacgaggccc tgggtggcac ggcttttgtt 2760
cagatgccgg cccacggcct attcccctgg tgcggcctgc tgctggatac ccggaccctg 2820
gaggtgcaga gcgactactc caggtgagcg cacctggccg gaagtggagc ctgtgcccgg 2880
ctggggcagg tgctgctgca gggccgttgc gtccacctct gcttccgtgt ggggcaggcg 2940
actgccaatc ccaaagggtc agatgccaca gggtgcccct cgtcccatct ggggctgagc 3000
acaaatgcat ctttctgtgg gagtgagggt gcctcacaac gggagcagtt ttctgtgcta 3060
ttttggtaa                                                        3069
```

<210> 42
<211> 948
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 3; Encoded by SEQ ID NO:41

<400> 42

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
             20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
         35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50                  55                  60
```

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

D10

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln

370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

D10

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
785 790 795 800

D10 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Arg
945

<210> 43
<211> 3362
<212> DNA
<213> Homo sapiens

<220>
<223> Altered C-terminus Protein; with Intron Alpha,
Beta and 3

<400> 43
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcgggggа gcggggcgtg ggggctgctg 420
ctgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggctg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
gacccgccgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacaccatc 2160
ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccccagaa cacgtactgc 2220
gtgcgtcggt atgccgtggt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280
agccacgtct ctaccttgac agacctccag ccgtacatgc gacagttcgt ggctcacctg 2340
caggagacca gcccgctgag ggatgccgtc gtcatcgagc agagctcctc cctgaatgag 2400
gccagcagtg gcctcttcga cgtcttccta cgcttcatgt gccaccacgc cgtgcgcatc 2460
aggggcaagt cctacgtcca gtgccagggg atcccgcagg gctccatcct ctccacgctg 2520
ctctgcagcc tgtgctacgg cgacatggag aacaagctgt ttgcggggat tcggcgggac 2580
gggctgctcc tgcgtttggt ggatgatttc ttgttggtga cacctcacct cacccacgcg 2640
aaaaccttcc tcaggaccct ggtccgaggt gtccctgagt atggctgcgt ggtgaacttg 2700
cggaagacag tggtgaactt ccctgtagaa gacgaggccc tgggtggcac ggcttttgtt 2760
cagatgccgg cccacggcct attcccctgg tgcggcctgc tgctggatac ccggaccctg 2820
gaggtgcaga gcgactactc cagctatgcc cggacctcca tcagagccag tctcaccttc 2880
aaccgcggct tcaaggctgg gaggaacatg cgtcgcaaac tctttggggt cttgcggctg 2940
aagtgtcaca gcctgtttct ggatttgcag gtgaacagcc tccagacggt gtgcaccaac 3000
atctacaaga tcctcctgct gcaggcgtac aggtttcacg catgtgtgct gcagctccca 3060
tttcatcagc aagtttggaa gaaccccaca tttttcctgc gcgtcatctc tgacacggcc 3120
tccctctgct actccatcct gaaagccaag aacgcagccg aagaaaacat ttctgtcgtg 3180

actcctgcgg tgcttgggtc gggacagcca gagatggagc caccccgcag accgtcgggt 3240
gtgggcagct ttccggtgtc tcctgggagg ggagttgggc tgggcctgtg actcctcagc 3300
ctctgttttc ccccagggat gtcgctgggg gccaagggcg ccgccggccc tctgccctcc 3360
ga 3362

<210> 44
<211> 1096
<212> PRT
<213> Homo sapiens

<220>
<223> Altered C-terminus Protein; Encoded by SEQ ID NO:43

<400> 44
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

D10

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
225 230 235 240

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
245 250 255

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
260 265 270

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
275 280 285

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
290 295 300

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
305 310 315 320

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
325 330 335

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
340 345 350

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
355 360 365

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
370 375 380

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
385 390 395 400

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
405 410 415

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
420 425 430

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
435 440 445

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
450 455 460

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
465 470 475 480

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
485 490 495

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
500 505 510

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
515 520 525

530 535 540

D10

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
645 650 655

D10

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
965 970 975

D10 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn
1045 1050 1055

Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met
1060 1065 1070

Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro
1075 1080 1085

Gly Arg Gly Val Gly Leu Gly Leu
1090 1095

<210> 45
<211> 3918
<212> DNA
<213> Homo sapiens

<220>
<223> Protein that lacks Motif A; with Intron Beta

<400> 45

atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcgggggа gcggggcgtg ggggctgctg 420
ctgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggctg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
gacccgccgc ctgagctgta ctttgtcaag gacaggctca cggaggtcat cgccagcatc 2160
atcaaacccc agaacacgta ctgcgtgcgt cggtatgccg tggtccagaa ggccgcccat 2220
gggcacgtcc gcaaggcctt caagagccac gtctctacct tgacagacct ccagccgtac 2280
atgcgacagt tcgtggctca cctgcaggag accagcccgc tgagggatgc cgtcgtcatc 2340
gagcagagct cctccctgaa tgaggccagc agtggcctct tcgacgtctt cctacgcttc 2400
atgtgccacc acgccgtgcg catcaggggc aagtcctacg tccagtgcca ggggatcccg 2460
cagggctcca tcctctccac gctgctctgc agcctgtgct acggcgacat ggagaacaag 2520
ctgtttgcgg ggattcggcg ggacgggctg ctcctgcgtt tggtggatga tttcttgttg 2580
gtgacacctc acctcaccca cgcgaaaacc ttcctcagga ccctggtccg aggtgtccct 2640
gagtatggct gcgtggtgaa cttgcggaag acagtggtga acttccctgt agaagacgag 2700
gccctgggtg gcacggcttt tgttcagatg ccggcccacg gcctattccc ctggtgcggc 2760
ctgctgctgg atacccggac cctggaggtg cagagcgact actccagcta tgcccggacc 2820
tccatcagag ccagtctcac cttcaaccgc ggcttcaagg ctgggaggaa catgcgtcgc 2880
aaactctttg gggtcttgcg gctgaagtgt cacagcctgt ttctggattt gcaggtgaac 2940
agcctccaga cggtgtgcac caacatctac aagatcctcc tgctgcaggc gtacaggttt 3000
cacgcatgtg tgctgcagct cccatttcat cagcaagttt ggaagaaccc cacatttttc 3060
ctgcgcgtca tctctgacac ggcctccctc tgctactcca tcctgaaagc caagaacgca 3120
gggatgtcgc tgggggccaa gggcgccgcc ggccctctgc cctccgaggc cgtgcagtgg 3180
ctgtgccacc aagcattcct gctcaagctg actcgacacc gtgtcaccta cgtgccactc 3240
ctggggtcac tcaggacagc ccagacgcag ctgagtcgga agctcccggg gacgacgctg 3300
actgccctgg aggccgcagc caacccggca ctgccctcag acttcaagac catcctggac 3360
tgatggccac ccgcccacag ccaggccgag agcagacacc agcagccctg tcacgccggg 3420
ctctacgtcc cagggaggga ggggcggccc acacccaggc ccgcaccgct gggagtctga 3480

D10

ggcctgagtg agtgtttggc cgaggcctgc atgtccggct gaaggctgag tgtccggctg 3540
aggcctgagc gagtgtccag ccaagggctg agtgtccagc acacctgccg tcttcacttc 3600
cccacaggct ggcgctcggc tccaccccag ggccagcttt tcctcaccag gagcccggct 3660
tccactcccc acataggaat agtccatccc cagattcgcc attgttcacc cctcgccctg 3720
ccctcctttg ccttccaccc ccaccatcca ggtggagacc ctgagaagga ccctgggagc 3780
tctgggaatt tggagtgacc aaaggtgtgc cctgtacaca ggcgaggacc ctgcacctgg 3840
atgggggtcc ctgtgggtca aattgggggg aggtgctgtg ggagtaaaat actgaatata 3900
tgagtttttc agttttga 3918

<210> 46
<211> 1120
<212> PRT
<213> Homo sapiens

<220>
<223> Protein that lacks Motif A; Encoded by SEQ ID NO:45

<400> 46
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335

D10

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys

```
        515                 520                 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
    530                 535                 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545                 550                 555                 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
                565                 570                 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
            580                 585                 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
        595                 600                 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
    610                 615                 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625                 630                 635                 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
                645                 650                 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
            660                 665                 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
        675                 680                 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
    690                 695                 700

Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
705                 710                 715                 720

Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
                725                 730                 735

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
            740                 745                 750

Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
        755                 760                 765

Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
    770                 775                 780

Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
785                 790                 795                 800

Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
                805                 810                 815

Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
            820                 825                 830
```

D10

Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
835 840 845

Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
850 855 860

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
865 870 875 880

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
885 890 895

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
900 905 910

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
915 920 925

Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
930 935 940

D10

Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
945 950 955 960

Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
965 970 975

Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
980 985 990

Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
995 1000 1005

Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
1010 1015 1020

Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
1025 1030 1035 1040

Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
1045 1050 1055

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
1060 1065 1070

His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
1075 1080 1085

Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
1090 1095 1100

Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1105 1110 1115 1120

<210> 47
<211> 3033
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein that lacks Motif A; with Introns Beta and 2

<400> 47
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcgggggа gcggggcgtg ggggctgctg 420
ctgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggctg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
gacccgccgc ctgagctgta ctttgtcaag gacaggctca cggaggtcat cgccagcatc 2160
atcaaacccc agaacacgta ctgcgtgcgt cggtatgccg tggtccagaa ggccgcccat 2220
gggcacgtcc gcaaggcctt caagagccac gtctctacct tgacagacct ccagccgtac 2280
atgcgacagt tcgtggctca cctgcaggag accagcccgc tgagggatgc cgtcgtcatc 2340
gagcagagct cctccctgaa tgaggccagc agtggcctct tcgacgtctt cctacgcttc 2400
atgtgccacc acgccgtgcg catcaggggc aagtcctacg tccagtgcca ggggatcccg 2460
cagggctcca tcctctccac gctgctctgc agcctgtgct acggcgacat ggagaacaag 2520
ctgtttgcgg ggattcggcg ggacgggctg ctcctgcgtt tggtggatga tttcttgttg 2580
gtgacacctc acctcaccca cgcgaaaacc ttcctcagga ccctggtccg aggtgtccct 2640
gagtatggct gcgtggtgaa cttgcggaag acagtggtga acttccctgt agaagacgag 2700
gccctgggtg gcacggcttt tgttcagatg ccggcccacg gcctattccc ctggtgcggc 2760
ctgctgctgg atacccggac cctggaggtg cagagcgact actccaggtg agcgcacctg 2820

D10

gccggaagtg gagcctgtgc ccggctgggg caggtgctgc tgcagggccg ttgcgtccac 2880
ctctgcttcc gtgtggggca ggcgactgcc aatcccaaag ggtcagatgc cacagggtgc 2940
ccctcgtccc atctggggct gagcacaaat gcatctttct gtgggagtga gggtgcctca 3000
caacgggagc agttttctgt gctattttgg taa 3033

<210> 48
<211> 936
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein that lacks Motif A; Encoded by
SEQ ID NO:47

<400> 48
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

D10

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg

225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350

D10

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
645 650 655

D10 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
690 695 700

Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
705 710 715 720

Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
725 730 735

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
740 745 750

Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
755 760 765

Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
770 775 780

Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
785 790 795 800

Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
805 810 815

Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
820 825 830

Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
835 840 845

```
Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
    850                 855                 860

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
865                 870                 875                 880

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
                885                 890                 895

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
            900                 905                 910

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
        915                 920                 925

Glu Val Gln Ser Asp Tyr Ser Arg
    930                 935
```

<210> 49
<211> 3326
<212> DNA
<213> Homo sapiens

D1D

<220>
<223> Protein Lacking Motif A and Altered C-Terminus;
with Introns Beta and 3

<400> 49

```
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcgggggа gcggggcgtg ggggctgctg 420
ctgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgtcccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020
ctgcggccct ccttcctact cagctctctg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320
gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc ccccaggcct ctggggctcc 1440
aggcacaacg aacgccgctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggctg 1560
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620
ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
```

```
tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800
ctgtcggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
ctccgcttca tccccaagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100
gacccgccgc ctgagctgta ctttgtcaag gacaggctca cggaggtcat cgccagcatc 2160
atcaaacccc agaacacgta ctgcgtgcgt cggtatgccg tggtccagaa ggccgcccat 2220
gggcacgtcc gcaaggcctt caagagccac gtctctacct tgacagacct ccagccgtac 2280
atgcgacagt tcgtggctca cctgcaggag accagcccgc tgagggatgc cgtcgtcatc 2340
gagcagagct cctccctgaa tgaggccagc agtggcctct tcgacgtctt cctacgcttc 2400
atgtgccacc acgccgtgcg catcaggggc aagtcctacg tccagtgcca ggggatcccg 2460
cagggctcca tcctctccac gctgctctgc agcctgtgct acggcgacat ggagaacaag 2520
ctgtttgcgg ggattcggcg ggacgggctg ctcctgcgtt tggtggatga tttcttgttg 2580
gtgacacctc acctcaccca cgcgaaaacc ttcctcagga ccctggtccg aggtgtccct 2640
gagtatggct gcgtggtgaa cttgcggaag acagtggtga acttccctgt agaagacgag 2700
gccctgggtg gcacggcttt tgttcagatg ccggcccacg gcctattccc ctggtgcggc 2760
ctgctgctgg atacccggac cctggaggtg cagagcgact actccagcta tgcccggacc 2820
tccatcagag ccagtctcac cttcaaccgc ggcttcaagg ctgggaggaa catgcgtcgc 2880
aaactctttg gggtcttgcg gctgaagtgt cacagcctgt ttctggattt gcaggtgaac 2940
agcctccaga cggtgtgcac caacatctac aagatcctcc tgctgcaggc gtacaggttt 3000
cacgcatgtg tgctgcagct cccatttcat cagcaagttt ggaagaaccc cacatttttc 3060
ctgcgcgtca tctctgacac ggcctccctc tgctactcca tcctgaaagc caagaacgca 3120
gccgaagaaa acatttctgt cgtgactcct gcggtgcttg ggtcgggaca gccagagatg 3180
gagccacccc gcagaccgtc gggtgtgggc agctttccgg tgtctcctgg gaggggagtt 3240
gggctgggcc tgtgactcct cagcctctgt tttcccccag ggatgtcgct gggggccaag 3300
ggcgccgccg gccctctgcc ctccga                                      3326
```

D18

<210> 50
<211> 1084
<212> PRT
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A and Altered C-Terminus;
Encoded by SEQ ID NO:49

<400> 50

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
             20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
         35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65                  70                  75                  80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
                 85                  90                  95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
            100                 105                 110
```

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

D10

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540

D10

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
690 695 700

Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
705 710 715 720

Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln

```
                725                 730                 735

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
            740                 745                 750

Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
        755                 760                 765

Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
    770                 775                 780

Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
785                 790                 795                 800

Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
                805                 810                 815

Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
            820                 825                 830

Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
        835                 840                 845

Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
    850                 855                 860

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
865                 870                 875                 880

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
                885                 890                 895

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
            900                 905                 910

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
        915                 920                 925

Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
    930                 935                 940

Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
945                 950                 955                 960

Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
                965                 970                 975

Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
            980                 985                 990

Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
        995                1000                1005

Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
   1010                1015                1020

Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
1025                1030                1035                1040
```

D10

Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly
1045 1050 1055

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
1060 1065 1070

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
1075 1080

<210> 51
<211> 2135
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1871)..(1873)
<223> Wherein N is A, C, G or T

<220>
<223> N-Terminal Truncated Telomerase (ver. 2); with Intron Y

D10

<400> 51
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagacccc 1440
gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgccccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat nnngacagtc accaggggggg ttgaccgccg gactgggcgt ccccagggtt 1920

gactatagga ccaggtgtcc aggtgccctg caagtagagg ggctctcaga ggcgtctggc 1980
tggcatgggt ggacgtggcc ccgggcatgg ccttctgcgt gtgctgccgt gggtgccctg 2040
agccctcact gagtcggtgg gggcttgtgg cttcccgtga gcttcccccc agtctgttgt 2100
ctggctgagc aagcctcctg aggggctctc tattg 2135

<210> 52
<211> 622
<212> PRT
<213> Homo sapiens

<220>
<223> N-Terminal Truncated Telomerase (ver.2); encoded
by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

D10

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser

```
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305                 310                 315                 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
                325                 330                 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
            340                 345                 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
        355                 360                 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
    370                 375                 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385                 390                 395                 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
                405                 410                 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
            420                 425                 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
        435                 440                 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
    450                 455                 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465                 470                 475                 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                 490                 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
            500                 505                 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
        515                 520                 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
    530                 535                 540
```

D10

```
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545                 550                 555                 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
                565                 570                 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
            580                 585                 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
        595                 600                 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
    610                 615                 620
```

<210> 53
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<223> Splicing Variant of Human Telomerase encoded by Intron Y, ORF2, berfore the termination codon. SEQ ID NOs: 51,55,59,63,67,71,75,79,83 encode this fragment

D10

<400> 53

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
             20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
         35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala
 65                  70                  75                  80

Ser Gly Trp Gly
```

<210> 54
<211> 537
<212> PRT
<213> Homo sapiens

<220>
<223> N-Terminal Truncated Telomerase (ver. 2); encoded by SEQ ID NO:51, with Y intron, ORF2, after the termination codon

<400> 54

```
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
  1               5                  10                  15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
            20                  25                  30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
        35                  40                  45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
    50                  55                  60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65                  70                  75                  80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
                85                  90                  95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
            100                 105                 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
        115                 120                 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
    130                 135                 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145                 150                 155                 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
                165                 170                 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
            180                 185                 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
        195                 200                 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
    210                 215                 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225                 230                 235                 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
                245                 250                 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
            260                 265                 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
        275                 280                 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
    290                 295                 300
```

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
420 425 430

D10

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly
530 535

<210> 55
<211> 2145
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein 1 (ver.2); with Introns Y and 1

<400> 55
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180

gacgcacggc cgcccccgc cgcccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggcccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagacccc 1440
gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgcccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggtggct gtgctttggt ttaacttcct ttttaaccag aagccgagcg 2100
tctcacctcg agggtgaagg cactgttcag cgtgctcaac tacga 2145

<210> 56
<211> 704
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 1 (ver.2); encoded by SEQ ID NO:55, with Y Intron ORF1

<400> 56
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

D10 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

D10 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu
675 680 685

Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly

690 695 700

<210> 57
<211> 619
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 1 (ver.2): encoded by SEQ ID NO:55, with Intron Y ORF2 after the termination codon

<400> 57
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

D12 Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
340 345 350

D10

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

```
Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
    530                 535                 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545                 550                 555                 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
                565                 570                 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
            580                 585                 590

Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe Thr Phe Leu
        595                 600                 605

Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
    610                 615


<210> 58
<211> 704
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 1 (ver.2); encoded by SEQ ID
      NO:55, with Intron Y ORF3

<400> 58
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
            20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
        35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
    50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65                  70                  75                  80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
                85                  90                  95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
        115                 120                 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160
```

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

D10 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

```
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465                 470                 475                 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                 490                 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
            500                 505                 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
        515                 520                 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
    530                 535                 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545                 550                 555                 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
                565                 570                 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
            580                 585                 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
        595                 600                 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
    610                 615                 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625                 630                 635                 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
                645                 650                 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
            660                 665                 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu
        675                 680                 685

Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
    690                 695                 700
```

<210> 59
<211> 2645
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein 2 (ver.2); with Intron Y and Alpha

<400> 59
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgccccccgc cgcccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagacccc 1440
gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgcccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
tgtactttgt caaggtggat gtgacgggcg cgtacgacac catcccccag gacaggctca 2280
cggaggtcat cgccagcatc atcaaacccc agaacacgta ctgcgtgcgt cggtatgccg 2340
tggtccagaa ggccgcccat gggcacgtcc gcaaggcctt caagagccac gtcctacgtc 2400
cagtgccagg ggatcccgca gggctccatc ctctccacgc tgctctgcag cctgtgctac 2460
ggcgacatgg agaacaagct gtttgcgggg attcggcggg acgggctgct cctgcgtttg 2520
gtggatgatt tcttgttggt gacacctcac ctcacccacg cgaaaacctt cctcaggacc 2580
ctggtccgag gtgtccctga gtatggctgc gtggtgaact tgcggaagac agtggtgaac 2640
ttccc 2645

<210> 60
<211> 841
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:59, with Intron Y ORF1

<400> 60
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser

```
1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
            20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
        35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
    50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65                  70                  75                  80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
                85                  90                  95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
        115                 120                 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165                 170                 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305                 310                 315                 320
```

D10

```
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
                325                 330                 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
            340                 345                 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
        355                 360                 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
    370                 375                 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385                 390                 395                 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
                405                 410                 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
            420                 425                 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
        435                 440                 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
    450                 455                 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465                 470                 475                 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                 490                 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
            500                 505                 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
        515                 520                 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
    530                 535                 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545                 550                 555                 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
                565                 570                 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
            580                 585                 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
        595                 600                 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
    610                 615                 620
```

D10

```
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625                 630                 635                 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
                645                 650                 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
            660                 665                 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
        675                 680                 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
    690                 695                 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705                 710                 715                 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
                725                 730                 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
            740                 745                 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
        755                 760                 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
    770                 775                 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro
785                 790                 795                 800

Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln
                805                 810                 815

Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala
            820                 825                 830

Gly Arg Ala Ala Pro Ala Phe Val Gly
        835                 840
```

D10

<210> 61
<211> 756
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:59 with Intron Y ORF2 after the termination codon

<400> 61

```
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
  1               5                  10                  15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
```

```
                20                  25                  30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
        35                  40                  45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
    50                  55                  60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65                  70                  75                  80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
                85                  90                  95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
            100                 105                 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
        115                 120                 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
    130                 135                 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145                 150                 155                 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
                165                 170                 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
            180                 185                 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
        195                 200                 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
    210                 215                 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225                 230                 235                 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
                245                 250                 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
            260                 265                 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
        275                 280                 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
    290                 295                 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305                 310                 315                 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
                325                 330                 335
```

D10

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
450 455 460

D10

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625 630 635 640

```
Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
                645                 650                 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
            660                 665                 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
        675                 680                 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
    690                 695                 700

Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro
705                 710                 715                 720

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
                725                 730                 735

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
            740                 745                 750

Ala Phe Val Gly
        755
```

D10

<210> 62
<211> 841
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO: 59 with Intron Y ORF3

<400> 62

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
            20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
        35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
    50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65                  70                  75                  80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
                85                  90                  95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
        115                 120                 125
```

```
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165                 170                 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305                 310                 315                 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
                325                 330                 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
            340                 345                 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
        355                 360                 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
    370                 375                 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385                 390                 395                 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
                405                 410                 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
            420                 425                 430
```

D10

```
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
        435                 440                 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
    450                 455                 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465                 470                 475                 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                 490                 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
            500                 505                 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
        515                 520                 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
    530                 535                 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545                 550                 555                 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
                565                 570                 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
            580                 585                 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
        595                 600                 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
    610                 615                 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625                 630                 635                 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
                645                 650                 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
            660                 665                 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
        675                 680                 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
    690                 695                 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705                 710                 715                 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
                725                 730                 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
```

D10

```
            740                 745                 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
        755                 760                 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
    770                 775                 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro
785                 790                 795                 800

Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln
                805                 810                 815

Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala
            820                 825                 830

Gly Arg Ala Ala Pro Ala Phe Val Gly
        835                 840
```

<210> 63
<211> 3500
<212> DNA
D10 <213> Homo sapiens

<220>
<223> Reference Protein (ver.2); with Introns Y, Alpha and Beta

<400> 63
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgttgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagacccc 1440
gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgccccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620

```
aggagctgac gtggaagatg agcgtgcggg gctgcgcttg gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
tgtactttgt caaggtggat gtgacgggcg cgtacgacac catcccccag gacaggctca 2280
cggaggtcat cgccagcatc atcaaacccc agaacacgta ctgcgtgcgt cggtatgccg 2340
tggtccagaa ggccgcccat gggcacgtcc gcaaggcctt caagagccac gtctctacct 2400
tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag accagcccgc 2460
tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc agtggcctct 2520
tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc aagtcctacg 2580
tccagtgcca ggggatcccg cagggctcca tcctctccac gctgctctgc agcctgtgct 2640
acggcgacat ggagaacaag ctgtttgcgg ggattcggcg ggacgggctg ctcctgcgtt 2700
tggtggatga tttcttgttg gtgacacctc acctcaccca cgcgaaaacc ttcctcagga 2760
ccctggtccg aggtgtccct gagtatggct gcgtggtgaa cttgcggaag acagtggtga 2820
acttccctgt agaagacgag gccctgggtg gcacggcttt tgttcagatg ccggcccacg 2880
gcctattccc ctggtgcggc ctgctgctgg atacccggac cctggaggtg cagagcgact 2940
actccagcta tgcccggacc tccatcagag ccagtctcac cttcaaccgc ggcttcaagg 3000
ctgggaggaa catgcgtcgc aaactctttg gggtcttgcg gctgaagtgt cacagcctgt 3060
ttctggattt gcaggtgaac agcctccaga cggtgtgcac caacatctac aagatcctcc 3120
tgctgcaggc gtacaggttt cacgcatgtg tgctgcagct cccatttcat cagcaagttt 3180
ggaagaaccc cacatttttc ctgcgcgtca tctctgacac ggcctccctc tgctactcca 3240
tcctgaaagc caagaacgca gggatgtcgc tgggggccaa gggcgccgcc ggccctctgc 3300
cctccgaggc cgtgcagtgg ctgtgccacc aagcattcct gctcaagctg actcgacacc 3360
gtgtcaccta cgtgccactc ctggggtcac tcaggacagc ccagacgcag ctgagtcgga 3420
agctcccggg gacgacgctg actgccctgg aggccgcagc caacccggca ctgccctcag 3480
acttcaagac catcctggac                                          3500
```

<210> 64
<211> 1165
<212> PRT
<213> Homo sapiens

<220>
<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
with Intron Y ORF1

<400> 64

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
             20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
         35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65                  70                  75                  80
```

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

D18

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu

385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Pro

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
785 790 795 800

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
805 810 815

Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
820 825 830

D10 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
835 840 845

His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
965 970 975

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
980 985 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
995 1000 1005

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
1010 1015 1020

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
1060 1065 1070

Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
1075 1080 1085

Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
1090 1095 1100

Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
1105 1110 1115 1120

Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
1125 1130 1135

D10

Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
1140 1145 1150

Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1155 1160 1165

<210> 65
<211> 1081
<212> PRT
<213> Homo sapiens

<220>
<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
with Intron Y ORF2 after the termination codon

<400> 65
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

D10

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

D10

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
645 650 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
690 695 700

Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro

```
705                 710                 715                 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
                725                 730                 735

Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
            740                 745                 750

Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
        755                 760                 765

Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
    770                 775                 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
785                 790                 795                 800

Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
                805                 810                 815

Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
            820                 825                 830

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
        835                 840                 845

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
    850                 855                 860

Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
865                 870                 875                 880

Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
                885                 890                 895

Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
            900                 905                 910

Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
        915                 920                 925

Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
    930                 935                 940

Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
945                 950                 955                 960

Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
                965                 970                 975

Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
            980                 985                 990

Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys
        995                1000                1005

Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His
   1010                1015                1020
```

D10

Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro
1025 1030 1035 1040

Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu
1045 1050 1055

Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu
1060 1065 1070

Pro Ser Asp Phe Lys Thr Ile Leu Asp
1075 1080

<210> 66
<211> 1165
<212> PRT
<213> Homo sapiens

<220>
<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
with Intron Y ORF3

<400> 66
D10 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu

```
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305                 310                 315                 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
                325                 330                 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
            340                 345                 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
        355                 360                 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
    370                 375                 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385                 390                 395                 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
                405                 410                 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
            420                 425                 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
        435                 440                 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
    450                 455                 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465                 470                 475                 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                 490                 495
```

D10

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

D10

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
785 790 795 800

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
805 810 815

Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
820 825 830

Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
835 840 845

His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
915 920 925

D10

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
965 970 975

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
980 985 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
995 1000 1005

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
1010 1015 1020

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
1060 1065 1070

Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
1075 1080 1085

Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
1090 1095 1100

Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val

1105 1110 1115 1120

Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
1125 1130 1135

Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
1140 1145 1150

Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1155 1160 1165

<210> 67
<211> 3173
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein (ver.2); with Introns Y, Alpha, Beta and 2

<400> 67
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggcccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gcccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagacccc 1440
gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgcccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160

```
tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
tgtactttgt caaggtggat gtgacgggcg cgtacgacac catcccccag gacaggctca 2280
cggaggtcat cgccagcatc atcaaacccc agaacacgta ctgcgtgcgt cggtatgccg 2340
tggtccagaa ggccgcccat gggcacgtcc gcaaggcctt caagagccac gtctctacct 2400
tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag accagcccgc 2460
tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc agtggcctct 2520
tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc aagtcctacg 2580
tccagtgcca ggggatcccg cagggctcca tcctctccac gctgctctgc agcctgtgct 2640
acggcgacat ggagaacaag ctgtttgcgg ggattcggcg ggacgggctg ctcctgcgtt 2700
tggtggatga tttcttgttg gtgacacctc acctcaccca cgcgaaaacc ttcctcagga 2760
ccctggtccg aggtgtccct gagtatggct gcgtggtgaa cttgcggaag acagtggtga 2820
acttccctgt agaagacgag gccctgggtg gcacggcttt tgttcagatg ccggcccacg 2880
gcctattccc ctggtgcggc ctgctgctgg atacccggac cctggaggtg cagagcgact 2940
actccaggtg agcgcacctg gccggaagtg gagcctgtgc ccggctgggg caggtgctgc 3000
tgcagggccg ttgcgtccac ctctgcttcc gtgtggggca ggcgactgcc aatcccaaag 3060
ggtcagatgc cacagggtgc ccctcgtccc atctggggct gagcacaaat gcatctttct 3120
gtgggagtga gggtgcctca caacgggagc agttttctgt gctattttgg taa        3173
```

<210> 68
<211> 982
<212> PRT
<213> Homo sapiens

D10

<220>
<223> Truncated Protein 3 (ver.2); encoded by SEQ ID NO:67 with Intron Y ORF1

<400> 68

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
             20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
         35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65                  70                  75                  80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
                 85                  90                  95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
        115                 120                 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160
```

```
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165                 170                 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305                 310                 315                 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
                325                 330                 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
            340                 345                 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
        355                 360                 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
    370                 375                 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385                 390                 395                 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
                405                 410                 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
            420                 425                 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
        435                 440                 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
    450                 455                 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
```

D10

```
465                 470                 475                 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                 490                 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
            500                 505                 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
        515                 520                 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
    530                 535                 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545                 550                 555                 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
                565                 570                 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
            580                 585                 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
        595                 600                 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
    610                 615                 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625                 630                 635                 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
                645                 650                 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
            660                 665                 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
        675                 680                 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
    690                 695                 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705                 710                 715                 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
                725                 730                 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
            740                 745                 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
        755                 760                 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
    770                 775                 780
```

D10

```
Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
785                 790                 795                 800

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
                805                 810                 815

Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
            820                 825                 830

Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
        835                 840                 845

His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
    850                 855                 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
865                 870                 875                 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
                885                 890                 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
            900                 905                 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
        915                 920                 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
    930                 935                 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
945                 950                 955                 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
                965                 970                 975

Gln Ser Asp Tyr Ser Arg
            980
```

<210> 69
<211> 897
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 3 (ver.2); encoded by SEQ ID NO:67 with Intron Y ORF2 after the termination codon

<400> 69

```
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
  1               5                  10                  15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
             20                  25                  30
```

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

D10 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys

```
            340                 345                 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
        355                 360                 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
    370                 375                 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385                 390                 395                 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
                405                 410                 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
            420                 425                 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
        435                 440                 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
    450                 455                 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465                 470                 475                 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
                485                 490                 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
            500                 505                 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
        515                 520                 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
    530                 535                 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545                 550                 555                 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
                565                 570                 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
            580                 585                 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
        595                 600                 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
    610                 615                 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625                 630                 635                 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
                645                 650                 655
```

D10

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
690 695 700

Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
725 730 735

Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
740 745 750

Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
755 760 765

D10

Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
785 790 795 800

Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
805 810 815

Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
820 825 830

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
835 840 845

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
850 855 860

Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
865 870 875 880

Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
885 890 895

Arg

<210> 70
<211> 982
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 3 (Ver.2); encoded by SEQ ID NO:67 with Intron Y ORF3

<400> 70

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
            20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
        35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
    50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65                  70                  75                  80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
                85                  90                  95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
        115                 120                 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165                 170                 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300
```

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

D10

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

D10

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
785 790 795 800

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
805 810 815

Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
820 825 830

Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
835 840 845

His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr

915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
965 970 975

Gln Ser Asp Tyr Ser Arg
980

<210> 71
<211> 3466
<212> DNA
<213> Homo sapiens

<220>
<223> Altered C-Terminus Protein (ver.2); with Introns Y, Alpha, Beta and 3

D10

<400> 71
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagaccccc 1440
gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgccccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980

```
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
tgtactttgt caaggtggat gtgacgggcg cgtacgacac catcccccag gacaggctca 2280
cggaggtcat cgccagcatc atcaaacccc agaacacgta ctgcgtgcgt cggtatgccg 2340
tggtccagaa ggccgcccat gggcacgtcc gcaaggcctt caagagccac gtctctacct 2400
tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag accagcccgc 2460
tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc agtggcctct 2520
tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc aagtcctacg 2580
tccagtgcca ggggatcccg cagggctcca tcctctccac gctgctctgc agcctgtgct 2640
acggcgacat ggagaacaag ctgtttgcgg ggattcggcg ggacgggctg ctcctgcgtt 2700
tggtggatga tttcttgttg gtgacacctc acctcaccca cgcgaaaacc ttcctcagga 2760
ccctggtccg aggtgtccct gagtatggct gcgtggtgaa cttgcggaag acagtggtga 2820
acttccctgt agaagacgag gccctgggtg gcacggcttt tgttcagatg ccggcccacg 2880
gcctattccc ctggtgcggc ctgctgctgg atacccggac cctggaggtg cagagcgact 2940
actccagcta tgcccggacc tccatcagag ccagtctcac cttcaaccgc ggcttcaagg 3000
ctgggaggaa catgcgtcgc aaactctttg gggtcttgcg gctgaagtgt cacagcctgt 3060
ttctggattt gcaggtgaac agcctccaga cggtgtgcac caacatctac aagatcctcc 3120
tgctgcaggc gtacaggttt cacgcatgtg tgctgcagct cccatttcat cagcaagttt 3180
ggaagaaccc cacatttttc ctgcgcgtca tctctgacac ggcctccctc tgctactcca 3240
tcctgaaagc caagaacgca gccgaagaaa acatttctgt cgtgactcct gcggtgcttg 3300
ggtcgggaca gccagagatg gagccacccc gcagaccgtc gggtgtgggc agctttccgg 3360
tgtctcctgg gaggggagtt gggctgggcc tgtgactcct cagcctctgt tttccccag 3420
ggatgtcgct gggggccaag ggcgccgccg gccctctgcc ctccga                3466
```

<210> 72
<211> 1130
<212> PRT
<213> Homo sapiens

<220>
<223> Altered C-Terminus Protein (ver.2); encoded by SEQ ID NO:71 with Intron Y ORF1

<400> 72

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
             20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
         35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65                  70                  75                  80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
                 85                  90                  95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
```

```
        115                 120                 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165                 170                 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305                 310                 315                 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
                325                 330                 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
            340                 345                 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
        355                 360                 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
    370                 375                 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385                 390                 395                 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
                405                 410                 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
            420                 425                 430
```

D10

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

D10

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
785 790 795 800

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
805 810 815

Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
820 825 830

Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
835 840 845

His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
865 870 875 880

D10

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
965 970 975

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
980 985 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
995 1000 1005

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
1010 1015 1020

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His

1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu
1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro
1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val
1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
1125 1130

<210> 73
<211> 1045
<212> PRT
<213> Homo sapiens

<220>
<223> Altered C-Terminus Protein (ver.2); encoded by SEQ ID NO:71 with Intron Y ORF2 after the termination codon

D10

<400> 73
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
275 280 285

D10

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
595 600 605

D10

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
645 650 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
690 695 700

Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
725 730 735

Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
740 745 750

Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
755 760 765

Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser

770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
785 790 795 800

Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
805 810 815

Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
820 825 830

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
835 840 845

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
850 855 860

Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
865 870 875 880

Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
885 890 895

Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
900 905 910

D10 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
915 920 925

Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
930 935 940

Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
945 950 955 960

Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
965 970 975

Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
980 985 990

Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn Ile Leu Val
995 1000 1005

Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met Glu Pro Pro
1010 1015 1020

Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro Gly Arg Gly
1025 1030 1035 1040

Val Gly Leu Gly Leu
1045

<210> 74
<211> 1130
<212> PRT
<213> Homo sapiens

<220>
<223> Altered C-Terminus Protein (ver.2); encoded by SEQ ID NO:71 with Intron Y ORF3

<400> 74

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
             20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
         35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65                  70                  75                  80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
                 85                  90                  95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
        115                 120                 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165                 170                 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
```

D10

275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

D10 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

D10

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
785 790 795 800

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
805 810 815

Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
820 825 830

Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
835 840 845

His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
965 970 975

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
980 985 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
995 1000 1005

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
1010 1015 1020

D10 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu
1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro
1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val
1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
1125 1130

<210> 75
<211> 4022
<212> DNA
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A (ver.2); with Introns Y
and Beta

<400> 75
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120

cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgccccccgc cgcccctctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggcccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagacccccc 1440
gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgcccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
tgtactttgt caaggacagg ctcacggagg tcatcgccag catcatcaaa ccccagaaca 2280
cgtactgcgt gcgtcggtat gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340
ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgcga cagttcgtgg 2400
ctcacctgca ggagaccagc ccgctgaggg atgccgtcgt catcgagcag agctcctccc 2460
tgaatgaggc cagcagtggc ctcttcgacg tcttcctacg cttcatgtgc caccacgccg 2520
tgcgcatcag gggcaagtcc tacgtccagt gccaggggat cccgcagggc tccatcctct 2580
ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640
ggcgggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
cccacgcgaa aaccttcctc aggaccctgg tccgaggtgt ccctgagtat ggctgcgtgg 2760
tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
cttttgttca gatgccggcc cacggcctat tcccctggtg cggcctgctg ctggataccc 2880
ggaccctgga ggtgcagagc gactactcca gctatgcccg gacctccatc agagccagtc 2940
tcaccttcaa ccgcggcttc aaggctggga ggaacatgcg tcgcaaactc tttggggtct 3000
tgcggctgaa gtgtcacagc ctgtttctgg atttgcaggt gaacagcctc cagacggtgt 3060
gcaccaacat ctacaagatc ctcctgctgc aggcgtacag gtttcacgca tgtgtgctgc 3120
agctcccatt tcatcagcaa gtttggaaga accccacatt tttcctgcgc gtcatctctg 3180
acacggcctc cctctgctac tccatcctga aagccaagaa cgcagggatg tcgctggggg 3240
ccaagggcgc cgccggccct ctgccctccg aggccgtgca gtggctgtgc caccaagcat 3300
tcctgctcaa gctgactcga caccgtgtca cctacgtgcc actcctgggg tcactcagga 3360
cagcccagac gcagctgagt cggaagctcc cggggacgac gctgactgcc ctggaggccg 3420
cagccaaccc ggcactgccc tcagacttca agaccatcct ggactgatgg ccacccgccc 3480
acagccaggc cgagagcaga caccagcagc cctgtcacgc cgggctctac gtcccaggga 3540
gggaggggcg gcccacaccc aggcccgcac cgctgggagt ctgaggcctg agtgagtgtt 3600

D10

tggccgaggc ctgcatgtcc ggctgaaggc tgagtgtccg gctgaggcct gagcgagtgt 3660
ccagccaagg gctgagtgtc cagcacacct gccgtcttca cttccccaca ggctggcgct 3720
cggctccacc ccagggccag cttttcctca ccaggagccc ggcttccact ccccacatag 3780
gaatagtcca tccccagatt cgccattgtt caccctcgc cctgccctcc tttgccttcc 3840
acccccacca tccaggtgga gaccctgaga aggaccctgg gagctctggg aatttggagt 3900
gaccaaaggt gtgccctgta cacaggcgag gaccctgcac ctggatgggg gtccctgtgg 3960
gtcaaattgg ggggaggtgc tgtgggagta aaatactgaa tatatgagtt tttcagtttt 4020
ga 4022

<210> 76
<211> 1154
<212> PRT
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID NO:75 with Intron Y ORF1

<400> 76
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

D10

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

D10

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe

515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

D10 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
755 760 765

Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
770 775 780

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
785 790 795 800

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
805 810 815

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
820 825 830

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
835 840 845

Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
850 855 860

Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
865 870 875 880

Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
885 890 895

Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
900 905 910

Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
915 920 925

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
945 950 955 960

D10 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
965 970 975

Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
980 985 990

Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
995 1000 1005

Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
1010 1015 1020

Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
1025 1030 1035 1040

Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
1045 1050 1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
1060 1065 1070

Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro
1075 1080 1085

Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu
1090 1095 1100

Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr
1105 1110 1115 1120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala
1125 1130 1135

Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile
1140 1145 1150

Leu Asp

<210> 77
<211> 1069
<212> PRT
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID NO:75 with Intron Y ORF2 after the termination codon

<400> 77
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

D1D Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro

```
     210                 215                 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225                 230                 235                 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
                245                 250                 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
            260                 265                 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
        275                 280                 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
    290                 295                 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305                 310                 315                 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
                325                 330                 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
            340                 345                 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
        355                 360                 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
    370                 375                 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385                 390                 395                 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
                405                 410                 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
            420                 425                 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
        435                 440                 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
    450                 455                 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465                 470                 475                 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
                485                 490                 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
            500                 505                 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
        515                 520                 525
```

D10

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
645 650 655

Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
660 665 670

DPD

Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala
675 680 685

His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
690 695 700

Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
705 710 715 720

Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
725 730 735

Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
740 745 750

His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
770 775 780

Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
785 790 795 800

Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His
805 810 815

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
820 825 830

```
Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
        835                 840                 845

Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
    850                 855                 860

Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
865                 870                 875                 880

Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
                885                 890                 895

Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
            900                 905                 910

Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val
        915                 920                 925

Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu
    930                 935                 940

Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
945                 950                 955                 960

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
                965                 970                 975

Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
            980                 985                 990

Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
        995                 1000                1005

Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
   1010                1015                1020

Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
1025                1030                1035                1040

Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
                1045                1050                1055

Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
            1060                1065
```

D10

<210> 78
<211> 1154
<212> PRT
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID NO:75 with Intron Y ORF3

<400> 78

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1                 5                  10                  15
```

```
His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
            20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
        35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
    50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65                  70                  75                  80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
                85                  90                  95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
        115                 120                 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165                 170                 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305                 310                 315                 320
```

D10

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

D10

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val

625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
755 760 765

D10 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
770 775 780

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
785 790 795 800

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
805 810 815

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
820 825 830

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
835 840 845

Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
850 855 860

Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
865 870 875 880

Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
885 890 895

Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
900 905 910

Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
915 920 925

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
930 935 940

```
Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
945                 950                 955                 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
                965                 970                 975

Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
            980                 985                 990

Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
        995                1000                1005

Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
   1010                1015                1020

Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
1025                1030                1035                1040

Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
               1045                1050                1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
           1060                1065                1070

Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro
       1075                1080                1085

Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu
   1090                1095                1100

Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr
1105                1110                1115                1120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala
               1125                1130                1135

Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile
           1140                1145                1150

Leu Asp
```

D10

<210> 79
<211> 3137
<212> DNA
<213> Homo sapiens

<220>
<223> Truncated Protein Lacking Motif A (ver.2); with
Introns Y, Beta and 2

<400> 79
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccccctcc ttccgccagg tgggcctccc cggggtcggc 240

gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagacccca 1440
gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgccccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
tgtactttgt caaggacagg ctcacggagg tcatcgccag catcatcaaa ccccagaaca 2280
cgtactgcgt gcgtcggtat gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340
ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgcga cagttcgtgg 2400
ctcacctgca ggagaccagc ccgctgaggg atgccgtcgt catcgagcag agctcctccc 2460
tgaatgaggc cagcagtggc ctcttcgacg tcttcctacg cttcatgtgc caccacgccg 2520
tgcgcatcag gggcaagtcc tacgtccagt gccaggggat cccgcagggc tccatcctct 2580
ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640
ggcgggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
cccacgcgaa aaccttcctc aggaccctgg tccgaggtgt ccctgagtat ggctgcgtgg 2760
tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
cttttgttca gatgccggcc cacggcctat tcccctggtg cggcctgctg ctggataccc 2880
ggaccctgga ggtgcagagc gactactcca ggtgagcgca cctggccgga agtggagcct 2940
gtgcccggct ggggcaggtg ctgctgcagg gccgttgcgt ccacctctgc ttccgtgtgg 3000
ggcaggcgac tgccaatccc aaagggtcag atgccacagg gtgcccctcg tcccatctgg 3060
ggctgagcac aaatgcatct ttctgtggga gtgagggtgc ctcacaacgg gagcagtttt 3120
ctgtgctatt ttggtaa 3137

D10

<210> 80
<211> 970
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein lacking Motif A (ver.2); encoded by SEQ ID NO:79 with Intron Y ORF1

<400> 80

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
            20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
        35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
    50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65                  70                  75                  80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
                85                  90                  95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
        115                 120                 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165                 170                 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300
```

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

D18

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

D10 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
755 760 765

Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
770 775 780

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
785 790 795 800

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
805 810 815

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
820 825 830

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
835 840 845

Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
850 855 860

Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
865 870 875 880

Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
885 890 895

Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
900 905 910

Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn

915 920 925

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg
965 970

<210> 81
<211> 885
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein lacking Motif A (ver.2); encoded by SEQ ID NO:79 with Intron Y ORF2 after the termination codon

<400> 81
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305 310 315 320

D10 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
610 615 620

D18 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
645 650 655

Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
660 665 670

Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala
675 680 685

His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
690 695 700

Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
705 710 715 720

Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
725 730 735

Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
740 745 750

His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
770 775 780

Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
785 790 795 800

Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His

805 810 815

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
820 825 830

Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
835 840 845

Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
850 855 860

Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
865 870 875 880

Ser Asp Tyr Ser Arg
885

<210> 82
<211> 970
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein lacking Motif A (ver.2); encoded by SEQ ID NO:79 with Intron Y ORF3

D10

<400> 82
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

D10 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg

```
465                 470                 475                 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                 490                 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
            500                 505                 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
        515                 520                 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
    530                 535                 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545                 550                 555                 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
                565                 570                 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
            580                 585                 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
        595                 600                 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
    610                 615                 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625                 630                 635                 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
                645                 650                 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
            660                 665                 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
        675                 680                 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
    690                 695                 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705                 710                 715                 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
                725                 730                 735

Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
            740                 745                 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
        755                 760                 765

Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
    770                 775                 780
```

D10

```
Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
785                 790                 795                 800

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
                805                 810                 815

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
            820                 825                 830

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
        835                 840                 845

Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
    850                 855                 860

Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
865                 870                 875                 880

Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
                885                 890                 895

Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
            900                 905                 910

Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
        915                 920                 925

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
    930                 935                 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
945                 950                 955                 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg
                965                 970
```

D10

<210> 83
<211> 3432
<212> DNA
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A and Altered C-Terminus
(ver.2); with Intron Y, Beta and 3

<400> 83
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccccgc cgcccccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600

gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagacccca 1440
gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgcccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
tgtactttgt caaggacagg ctcacggagg tcatcgccag catcatcaaa ccccagaaca 2280
cgtactgcgt gcgtcggtat gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340
ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgcga cagttcgtgg 2400
ctcacctgca ggagaccagc ccgctgaggg atgccgtcgt catcgagcag agctcctccc 2460
tgaatgaggc cagcagtggc ctcttcgacg tcttcctacg cttcatgtgc caccacgccg 2520
tgcgcatcag gggcaagtcc tacgtccagt gccaggggat cccgcagggc tccatcctct 2580
ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640
ggcgggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
cccacgcgaa aaccttcctc aggaccctgg tccgaggtgt ccctgagtat ggctgcgtgg 2760
tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
cttttgttca gatgccggcc cacggcctat tcccctggtg cggcctgctg ctggataccc 2880
ggaccctgga ggtgcagagc gactactcca gctatgcccg gacctccatc agagccagtc 2940
tcaccttcaa ccgcggcttc aaggctggga ggaacatgcg tcgcaaactc tttggggtct 3000
tgcggctgaa gtgtcacagc ctgtttctgg atttgcaggt gaacagcctc cagacggtgt 3060
gcaccaacat ctacaagatc ctcctgctgc aggcgtacag gtttcacgca tgtgtgctgc 3120
agctcccatt tcatcagcaa gtttggaaga accccacatt tttcctgcgc gtcatctctg 3180
acacggcctc cctctgctac tccatcctga aagccaagaa cgcagccgaa gaaaacattt 3240
ctgtcgtgac tcctgcggtg cttgggtcgg gacagccaga gatggagcca ccccgcagac 3300
cgtcgggtgt gggcagcttt ccggtgtctc ctgggagggg agttgggctg ggcctgtgac 3360
tcctcagcct ctgttttccc ccagggatgt cgctgggggc caagggcgcc gccggccctc 3420
tgccctccga ga 3432

<210> 84
<211> 1122
<212> PRT
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A and Altered C-Terminus
(ver.2); encoded by SEQ ID NO:83 with Intron Y
ORF1

<400> 84

```
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1               5                  10                  15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
            20                  25                  30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
        35                  40                  45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
    50                  55                  60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65                  70                  75                  80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
                85                  90                  95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
            100                 105                 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
        115                 120                 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130                 135                 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145                 150                 155                 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165                 170                 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
            180                 185                 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300
```

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

D10

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
755 760 765

P10

Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
770 775 780

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
785 790 795 800

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
805 810 815

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
820 825 830

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
835 840 845

Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
850 855 860

Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
865 870 875 880

Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
885 890 895

Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
900 905 910

Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn

915 920 925

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
965 970 975

Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
980 985 990

Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
995 1000 1005

Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
1010 1015 1020

Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
1025 1030 1035 1040

Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
1045 1050 1055

D10 Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
1060 1065 1070

Asn Ala Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
1075 1080 1085

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
1090 1095 1100

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile
1105 1110 1115 1120

Gly Ala

<210> 85
<211> 1037
<212> PRT
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A and Altered C-Terminus
(ver.2); encoded by SEQ ID NO:83 with Intron Y
ORF2 after the termination codon

<400> 85
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

D10

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

D10 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr

645 650 655

Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
660 665 670

Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala
675 680 685

His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
690 695 700

Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
705 710 715 720

Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
725 730 735

Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
740 745 750

His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
770 775 780

Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
785 790 795 800

D10 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His
805 810 815

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
820 825 830

Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
835 840 845

Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
850 855 860

Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
865 870 875 880

Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
885 890 895

Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
900 905 910

Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val
915 920 925

Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu
930 935 940

Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
945 950 955 960

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
965 970 975

Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu
980 985 990

Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu
995 1000 1005

Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser
1010 1015 1020

Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile Gly Ala
1025 1030 1035

<210> 86
<211> 1122
<212> PRT
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A and Altered C-Terminus (ver.2); encoded by SEQ ID NO:83 with Intron Y ORF3

<400> 86
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

D10

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg

```
465                 470                 475                 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                 490                 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
            500                 505                 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
        515                 520                 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
    530                 535                 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545                 550                 555                 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
                565                 570                 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
            580                 585                 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
        595                 600                 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
    610                 615                 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625                 630                 635                 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
                645                 650                 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
            660                 665                 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
        675                 680                 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
    690                 695                 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705                 710                 715                 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
                725                 730                 735

Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
            740                 745                 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
        755                 760                 765

Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
    770                 775                 780
```

D10

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
785 790 795 800

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
805 810 815

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
820 825 830

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
835 840 845

Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
850 855 860

Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
865 870 875 880

Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
885 890 895

Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
900 905 910

Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
915 920 925

D/D Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
965 970 975

Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
980 985 990

Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
995 1000 1005

Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
1010 1015 1020

Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
1025 1030 1035 1040

Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
1045 1050 1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
1060 1065 1070

Asn Ala Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
1075 1080 1085

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
1090 1095 1100

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile
1105 1110 1115 1120

Gly Ala

<210> 87
<211> 7615
<212> DNA
<213> Homo sapiens

<220>
<223> Human Telomerase Clone with Exon Beta Spliced Out

<400> 87
tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa 60
aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttcgc cagctggcgt 120
aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa 180
tggcgcctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat 240
tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag 300
aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc 360
catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc 420
gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct 480
ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag 540
cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgccataaa 600
ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggccttttt gcgtttctac 660
aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc 720
gtttttgcat caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg 780
ccgcatagtt aagccagccc cgacacccgc caacacccgc tgacgcgccc tgacgggctt 840
gtctgctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc 900
agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat 960
ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca 1020
ccatcgaatg gtgcaaaacc tttcgcggta tggcatgata gcgcccggaa gagagtcaat 1080
tcagggtggt gaatgtgaaa ccagtaacgt tatacgatgt cgcagagtat gccggtgtct 1140
cttatcagac cgtttcccgc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg 1200
aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac 1260
tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc 1320
cgtcgcaaat tgtcgcggcg attaaatctc gcgccgatca actgggtgcc agcgtggtgg 1380
tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaagc ggcggtgcac aatcttctcg 1440
cgcaacgcgt cagtgggctg atcattaact atccgctgga tgaccaggat gccattgctg 1500
tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacaccca 1560
tcaacagtat tattttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg 1620
cattgggtca ccagcaaatc gcgctgttag cgggcccatt aagttctgtc tcggcgcgtc 1680
tgcgtctggc tggctggcat aaatatctca ctcgcaatca aattcagccg atagcggaac 1740
gggaaggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg 1800
gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg 1860
ccattaccga gtccgggctg cgcgttggtg cggatatctc ggtagtggga tacgacgata 1920
ccgaagacag ctcatgttat atcccgccgt taaccaccat caaacaggat tttcgcctgc 1980
tggggcaaac cagcgtggac cgcttgctgc aactctctca gggccaggcg gtgaagggca 2040
atcagctgtt gcccgtctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa 2100
ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac 2160
tggaaagcgg gcagtgagcg caacgcaatt aatgtaagtt agctcactca ttaggcaccc 2220
caggctttac actttatgct tccgacctgc aagaacctca cgtcaggtgg cacttttcgg 2280
ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg 2340

ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt 2400
attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt 2460
gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg 2520
ggttacatcg agaactggat ctcaacagcg gtaagatcct tgagagtttt cgccccgaag 2580
aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgta 2640
ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg 2700
agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca 2760
gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag 2820
gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact cgccttgatc 2880
gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg 2940
tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact ctagcttccc 3000
ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt ctgcgctcgg 3060
cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt gggtctcgcg 3120
gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt atctacacga 3180
cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac 3240
tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag attgatttaa 3300
aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca 3360
aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag 3420
gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac 3480
cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt ccgaaggtaa 3540
ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg tagttaggcc 3600
accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaatc ctgttaccag 3660
tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac 3720
cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc agcttggagc 3780
gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc 3840
ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca ggagagcgca 3900
cgagggagct tccagggga aacgcctggt atctttatag tcctgtcggg tttcgccacc 3960
tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta tggaaaaacg 4020
ccagcaacgc ggcctttta cggttcctgg ccttttgctg gccttttgct cacatgttct 4080
ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag tgagctgata 4140
ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa gcggaagagc 4200
gcccaatacg caaaccgcct ctccccgcgc gttggccgat tcattaatgc agaattaatt 4260
ctcatgtttg acagcttatc atcgactgca cggtgcacca atgcttctgg cgtcaggcag 4320
ccatcggaag ctgtggtatg gctgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc 4380
aaggcgcact cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa 4440
tattctgaaa tgagctgttg acaattaatc atcggctcgt ataatgtgtg gaattgtgag 4500
cggataacaa tttcacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg 4560
tggcccgagt gctgcagagg ctgtgcgagc gcggcgcgaa gaacgtgctg gccttcggct 4620
tcgcgctgct ggacggggcc cgcgggggcc cccccgaggc cttcaccacc agcgtgcgca 4680
gctacctgcc caacacggtg accgacgcac tgcgggggag cggggcgtgg gggctgctgc 4740
tgcgccgcgt gggcgacgac gtgctggttc acctgctggc acgctgcgcg ctctttgtgc 4800
tggtggctcc cagctgcgcc taccaggtgt gcgggccgcc gctgtaccag ctcggcgctg 4860
ccactcaggc ccggcccccg ccacacgcta gtggaccccg aaggcgtctg ggatgcgaac 4920
gggcctggaa ccatagcgtc agggaggccg gggtcccccc gggcctgcca gccccgggtg 4980
cgaggaggcg cgggggcagt gccagccgaa gtctgccgtt gcccaagagg cccaggcgtg 5040
gcgctgcccc tgagccggag cggacgcccg ttgggcaggg gtcctgggcc cacccgggca 5100
ggacgcgtgg accgagtgac cgtggtttct gtgtggtgtc acctgccaga cccgccgaag 5160
aagccacctc tttggagggt gcgctctctg gcacgcgcca ctcccaccca tccgtgggcc 5220
gccagcacca cgcgggcccc ccatccacat cgcggccacc acgtccctgg gacacgcctt 5280
gtcccccggt gtacgccgag accaagcact tcctctactc ctcaggcgac aaggagcagc 5340
tgcggccctc cttcctactc agctctctga ggcccagcct gactggcgct cggaggctcg 5400
tggagaccat ctttctgggt tccaggccct ggatgccagg gactccccgc aggttgcccc 5460
gcctgcccca gcgctactgg caaatgcggc ccctgtttct ggagctgctt gggaaccacg 5520
cgcagtgccc ctacggggtg ctcctcaaga cgcactgccc gctgcgagct gcggtcaccc 5580
cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg 5640
aggacacaga cccccgtcgc ctggtgcagc tgctccgcca gcacagcagc ccctggcagg 5700
tgtacggctt cgtgcgggcc tgcctgcgcc ggctggtgcc cccaggcctc tggggctcca 5760
ggcacaacga acgccgcttc ctcaggaaca ccaagaagtt catctccctg gggaagcatg 5820

D10

ccaagctctc gctgcaggag ctgacgtgga agatgagcgt gcgggactgc gcttggctgc 5880
gcaggagccc aggggttggc tgtgttccgg ccgcagagca ccgtctgcgt gaggagatcc 5940
tggccaagtt cctgcactgg ctgatgagtg tgtacgtcgt cgagctgctc aggtctttct 6000
tttatgtcac ggagaccacg tttcaaaaga acaggctctt tttctaccgg aagagtgtct 6060
ggagcaagtt gcaaagcatt ggaatcagac agcacttgaa gagggtgcag ctgcgggagc 6120
tgtcggaagc agaggtcagg cagcatcggg aagccaggcc cgccctgctg acgtccagac 6180
tccgcttcat ccccaagcct gacgggctgc ggccgattgt gaacatggac tacgtcgtgg 6240
gagccagaac gttccgcaga gaaaagaggg ccgagcgtct cacctcgagg gtgaaggcac 6300
tgttcagcgt gctcaactac gagcgggcgc ggcgccccgg cctcctgggc gcctctgtgc 6360
tgggcctgga cgatatccac agggcctggc gcaccttcgt gctgcgtgtg cgggcccagg 6420
acccgccgcc tgagctgtac tttgtcaagg tggatgtgac gggcgcgtac gacaccatcc 6480
cccaggacag gctcacggag gtcatcgcca gcatcatcaa accccagaac acgtactgcg 6540
tgcgtcggta tgccgtggtc cagaaggccg cccatgggca cgtccgcaag gccttcaaga 6600
gccacgtcct acgtccagtg ccaggggatc ccgcagggct ccatcctctc cacgctgctc 6660
tgcagcctgt gctacggcga catggagaac aagctgtttg cggggattcg gcgggacggg 6720
ctgctcctgc gtttggtgga tgatttcttg ttggtgacac ctcacctcac ccacgcgaaa 6780
acttcctcag gacctggtcc gaagtgtcct gagtatggct gcgtggtgaa cttgcggaag 6840
acagtggtga acttccctgt agaagacgaa gccctgggtg gcacggcttt tgttcagatg 6900
ccggcccacg gcctattccc ctggtgcggc ctgctgctgg atacccggac cctggaggtg 6960
cagagcgact actccagcta tgcccggacc tccatcagag ccagtctcac cttcaaccgc 7020
ggcttcaagg ctgggaggaa catgcgtcgc aaactctttg gggtcttgcg gctgaagtgt 7080
cacagcctgt ttctggattt gcaggtgaac agcctccaga cggtgtgcac caacatctac 7140
aagatcctcc tgctgcaggc gtacaggttt cacgcatgtg tgctgcagct cccatttcat 7200
cagcaagttt ggaagaaccc cacatttttc ctgcgcgtca tctctgacac ggcctccctc 7260
tgctactcca tcctgaaagc caagaacgca gccgaagaaa acatttctgt cgtgactcct 7320
gcggtgcttg ggtcgggaca gccagagatg gagccacccc gcagaccgtc gggtgtgggc 7380
agctttccgg tgtctcctgg gaggggagtt gggctgggcc tgtgactcct cagcctctgt 7440
tttcccccag ggatgtcgct gggggccaag ggcgccgccg gccctctgcc ctccgaggcc 7500
gtgcagtggc tgtgccacca agcattcctg ctcaagctga ctcgacaccg tgtcacctac 7560
gtgccactcc tggggtcact caggacaggc aagtgtgggt ggaggccagt gcggg 7615

DD

<210> 88
<211> 7797
<212> DNA
<213> Homo sapiens

<220>
<223> Human Telomerase Clone with Alternative C-terminus

<400> 88
tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa 60
aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttcgc cagctggcgt 120
aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa 180
tggcgcctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat 240
tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag 300
aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc 360
catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc 420
gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct 480
ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag 540
cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgccataaa 600
ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggccttttt gcgtttctac 660
aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc 720
gtttttgcat caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg 780
ccgcatagtt aagccagccc cgacacccgc caacacccgc tgacgcgccc tgacgggctt 840
gtctgctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc 900
agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat 960
ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca 1020
ccatcgaatg gtgcaaaacc tttcgcggta tggcatgata gcgcccggaa gagagtcaat 1080

tcagggtggt gaatgtgaaa ccagtaacgt tatacgatgt cgcagagtat gccggtgtct 1140
cttatcagac cgtttcccgc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg 1200
aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac 1260
tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc 1320
cgtcgcaaat tgtcgcggcg attaaatctc gcgccgatca actgggtgcc agcgtggtgg 1380
tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaagc ggcggtgcac aatcttctcg 1440
cgcaacgcgt cagtgggctg atcattaact atccgctgga tgaccaggat gccattgctg 1500
tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacaccca 1560
tcaacagtat tattttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg 1620
cattgggtca ccagcaaatc gcgctgttag cgggcccatt aagttctgtc tcggcgcgtc 1680
tgcgtctggc tggctggcat aaatatctca ctcgcaatca aattcagccg atagcggaac 1740
gggaaggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg 1800
gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg 1860
ccattaccga gtccgggctg cgcgttggtg cggatatctc ggtagtggga tacgacgata 1920
ccgaagacag ctcatgttat atcccgccgt taaccaccat caaacaggat tttcgcctgc 1980
tggggcaaac cagcgtggac cgcttgctgc aactctctca gggccaggcg gtgaagggca 2040
atcagctgtt gcccgtctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa 2100
ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac 2160
tggaaagcgg gcagtgagcg caacgcaatt aatgtaagtt agctcactca ttaggcaccc 2220
caggctttac actttatgct tccgacctgc aagaacctca cgtcaggtgg cacttttcgg 2280
ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg 2340
ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt 2400
attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt 2460
gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg 2520
ggttacatcg agaactggat ctcaacagcg gtaagatcct tgagagtttt cgccccgaag 2580
aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgta 2640
ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg 2700
agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca 2760
gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag 2820
gaccgaagga gctaaccgct tttttgcaca acatgggggа tcatgtaact cgccttgatc 2880
gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg 2940
tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact ctagcttccc 3000
ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt ctgcgctcgg 3060
cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt gggtctcgcg 3120
gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt atctacacga 3180
cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac 3240
tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag attgatttaa 3300
aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca 3360
aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag 3420
gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac 3480
cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt ccgaaggtaa 3540
ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg tagttaggcc 3600
accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaatc ctgttaccag 3660
tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac 3720
cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc agcttggagc 3780
gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc 3840
ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca ggagagcgca 3900
cgagggagct tccagggggа aacgcctggt atctttatag tcctgtcggg tttcgccacc 3960
tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta tggaaaaacg 4020
ccagcaacgc ggcctttttа cggttcctgg ccttttgctg gccttttgct cacatgttct 4080
ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag tgagctgata 4140
ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa gcggaagagc 4200
gcccaatacg caaaccgcct ctccccgcgc gttggccgat tcattaatgc agaattaatt 4260
ctcatgtttg acagcttatc atcgactgca cggtgcacca atgcttctgg cgtcaggcag 4320
ccatcggaag ctgtggtatg gctgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc 4380
aaggcgcact cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa 4440
tattctgaaa tgagctgttg acaattaatc atcggctcgt ataatgtgtg gaattgtgag 4560
cggataacaa tttcacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg 4560

D10

tggcccgagt gctgcagagg ctgtgcgagc gcggcgcgaa gaacgtgctg gccttcggct 4620
tcgcgctgct ggacggggcc cgcgggggcc cccccgaggc cttcaccacc agcgtgcgca 4680
gctacctgcc caacacggtg accgacgcac tgcgggggag cggggcgtgg gggctgctgc 4740
tgcgccgcgt gggcgacgac gtgctggttc acctgctggc acgctgcgcg ctctttgtgc 4800
tggtggctcc cagctgcgcc taccaggtgt gcgggccgcc gctgtaccag ctcggcgctg 4860
ccactcaggc ccggcccccg ccacacgcta gtggaccccg aaggcgtctg ggatgcgaac 4920
gggcctggaa ccatagcgtc agggaggccg gggtccccct gggcctgcca gccccgggtg 4980
cgaggaggcg cgggggcagt gccagccgaa gtctgccgtt gcccaagagg cccaggcgtg 5040
gcgctgcccc tgagccggag cggacgcccg ttgggcaggg gtcctgggcc cacccgggca 5100
ggacgcgtgg accgagtgac cgtggtttct gtgtggtgtc acctgccaga cccgccgaag 5160
aagccacctc tttggagggt gcgctctctg gcacgcgcca ctcccaccca tccgtgggcc 5220
gccagcacca cgcgggcccc ccatccacat cgcggccacc acgtccctgg gacacgcctt 5280
gtcccccggt gtacgccgag accaagcact tcctctactc ctcaggcgac aaggagcagc 5340
tgcggccctc cttcctactc agctctctga ggcccagcct gactggcgct cggaggctcg 5400
tggagaccat ctttctgggt tccaggccct ggatgccagg gactccccgc aggttgcccc 5460
gcctgcccca gcgctactgg caaatgcggc ccctgtttct ggagctgctt gggaaccacg 5520
cgcagtgccc ctacggggtg ctcctcaaga cgcactgccc gctgcgagct gcggtcaccc 5580
cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg 5640
aggacacaga cccccgtcgc ctggtgcagc tgctccgcca gcacagcagc ccctggcagg 5700
tgtacggctt cgtgcgggcc tgcctgcgcc ggctggtgcc cccaggcctc tggggctcca 5760
ggcacaacga acgccgcttc ctcaggaaca ccaagaagtt catctccctg gggaagcatg 5820
ccaagctctc gctgcaggag ctgacgtgga agatgagcgt gcgggactgc gcttggctgc 5880
gcaggagccc aggggttggc tgtgttccgg ccgcagagca ccgtctgcgt gaggagatcc 5940
tggccaagtt cctgcactgg ctgatgagtg tgtacgtcgt cgagctgctc aggtctttct 6000
tttatgtcac ggagaccacg tttcaaaaga acaggctctt tttctaccgg aagagtgtct 6060
ggagcaagtt gcaaagcatt ggaatcagac agcacttgaa gagggtgcag ctgcgggagc 6120
tgtcggaagc agaggtcagg cagcatcggg aagccaggcc cgccctgctg acgtccagac 6180
tccgcttcat ccccaagcct gacgggctgc ggccgattgt gaacatggac tacgtcgtgg 6240
gagccagaac gttccgcaga gaaaagaggg ccgagcgtct cacctcgagg gtgaaggcac 6300
tgttcagcgt gctcaactac gagcgggcgc ggcgccccgg cctcctgggc gcctctgtgc 6360
tgggcctgga cgatatccac agggcctggc gcaccttcgt gctgcgtgtg cgggcccagg 6420
acccgccgcc tgagctgtac tttgtcaagg tggatgtgac gggcgcgtac gacaccatcc 6480
cccaggacag gctcacggag gtcatcgcca gcatcatcaa accccagaac acgtactgcg 6540
tgcgtcggta tgccgtggtc cagaaggccg cccatgggca cgtccgcaag gccttcaaga 6600
gccacgtctc taccttgaca gacctccagc cgtacatgcg acagttcgtg gctcacctgc 6660
aggagaccag cccgctgagg gatgccgtcg tcatcgagca gagctcctcc ctgaatgagg 6720
ccagcagtgg cctcttcgac gtcttcctac gcttcatgtg ccaccacgcc gtgcgcatca 6780
ggggcaagtc ctacgtccag tgccagggga tcccgcaggg ctccatcctc tccacgctgc 6840
tctgcagcct gtgctacggc gacatggaga acaagctgtt tgcggggatt cggcgggacg 6900
ggctgctcct gcgtttggtg gatgatttct tgttggtgac acctcacctc acccacgcga 6960
aaacttcctc aggacctggt ccgaagtgtc ctgagtatgg ctgcgtggtg aacttgcgga 7020
agacagtggt gaacttccct gtagaagacg aagccctggg tggcacggct tttgttcaga 7080
tgccggccca cggcctattc ccctggtgcg gcctgctgct ggataccgg accctggagg 7140
tgcagagcga ctactccagc tatgcccgga cctccatcag agccagtctc accttcaacc 7200
gcggcttcaa ggctgggagg aacatgcgtc gcaaactctt tggggtcttg cggctgaagt 7260
gtcacagcct gtttctggat ttgcaggtga acagcctcca gacggtgtgc accaacatct 7320
acaagatcct cctgctgcag gcgtacaggt ttcacgcatg tgtgctgcag ctcccatttc 7380
atcagcaagt ttggaagaac cccacatttt tcctgcgcgt catctctgac acggcctccc 7440
tctgctactc catcctgaaa gccaagaacg cagccgaaga aaacatttct gtcgtgactc 7500
ctgcggtgct tgggtcggga cagccagaga tggagccacc ccgcagaccg tcgggtgtgg 7560
gcagctttcc ggtgtctcct gggaggggag ttgggctggg cctgtgactc ctcagcctct 7620
gttttccccc agggatgtcg ctgggggcca agggcgccgc cggccctctg ccctccgagg 7680
ccgtgcagtg gctgtgccac caagcattcc tgctcaagct gactcgacac cgtgtcacct 7740
acgtgccact cctggggtca ctcaggacag gcaagtgtgg gtggaggcca gtgcggg 7797

<210> 89
<211> 7688
<212> DNA

D10

<213> Homo sapiens

<220>
<223> Human Telomerase Clone with exon Alpha Spliced Out

<400> 89
tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa 60
aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttcgc cagctggcgt 120
aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa 180
tggcgcctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat 240
tccctgtttt ggcggatgag agaagatttt cagcctgata cagattaaat cagaacgcag 300
aagcggtctg ataaaacaga atttgcctgg cggcagtagc gcggtggtcc cacctgaccc 360
catgccgaac tcagaagtga aacgccgtag cgccgatggt agtgtggggt ctccccatgc 420
gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct 480
ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag 540
cggatttgaa cgttgcgaag caacggcccg gagggtggcg ggcaggacgc ccgccataaa 600
ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggccttttt gcgtttctac 660
aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc 720
gtttttgcat caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg 780
ccgcatagtt aagccagccc cgacacccgc caacacccgc tgacgcgccc tgacgggctt 840
gtctgctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc 900
agaggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat 960
ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca 1020
ccatcgaatg gtgcaaaacc tttcgcggta tggcatgata gcgcccggaa gagagtcaat 1080
tcagggtggt gaatgtgaaa ccagtaacgt tatacgatgt cgcagagtat gccggtgtct 1140
cttatcagac cgtttcccgc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg 1200
aaaaagtgga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac 1260
tggcgggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc 1320
cgtcgcaaat tgtcgcggcg attaaatctc gcgccgatca actgggtgcc agcgtggtgg 1380
tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaagc ggcggtgcac aatcttctcg 1440
cgcaacgcgt cagtgggctg atcattaact atccgctgga tgaccaggat gccattgctg 1500
tggaagctgc ctgcactaat gttccggcgt tatttcttga tgtctctgac cagacaccca 1560
tcaacagtat tattttctcc catgaagacg gtacgcgact gggcgtggag catctggtcg 1620
cattgggtca ccagcaaatc gcgctgttag cgggcccatt aagttctgtc tcggcgcgtc 1680
tgcgtctggc tggctggcat aaatatctca ctcgcaatca aattcagccg atagcggaac 1740
gggaaggcga ctggagtgcc atgtccggtt ttcaacaaac catgcaaatg ctgaatgagg 1800
gcatcgttcc cactgcgatg ctggttgcca acgatcagat ggcgctgggc gcaatgcgcg 1860
ccattaccga gtccgggctg cgcgttggtg cggatatctc ggtagtggga tacgacgata 1920
ccgaagacag ctcatgttat atcccgccgt taaccaccat caaacaggat tttcgcctgc 1980
tggggcaaac cagcgtggac cgcttgctgc aactctctca gggccaggcg gtgaagggca 2040
atcagctgtt gcccgtctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa 2100
ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac 2160
tggaaagcgg gcagtgagcg caacgcaatt aatgtaagtt agctcactca ttaggcaccc 2220
caggctttac actttatgct tccgacctgc aagaacctca cgtcaggtgg cacttttcgg 2280
ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg 2340
ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt 2400
attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt 2460
gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg 2520
ggttacatcg agaactggat ctcaacagcg gtaagatcct tgagagtttt cgccccgaag 2580
aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgta 2640
ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat gacttggttg 2700
agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca 2760
gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca acgatcggag 2820
gaccgaagga gctaaccgct tttttgcaca acatgggggga tcatgtaact cgccttgatc 2880
gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg 2940
tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact ctagcttccc 3000
ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt ctgcgctcgg 3060
cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt gggtctcgcg 3120

D10

gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt atctacacga 3180
cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac 3240
tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag attgatttaa 3300
aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat ctcatgacca 3360
aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag 3420
gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac 3480
cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt ccgaaggtaa 3540
ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg tagttaggcc 3600
accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaatc ctgttaccag 3660
tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac 3720
cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc agcttggagc 3780
gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc 3840
ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca ggagagcgca 3900
cgagggagct tccagggga aacgcctggt atctttatag tcctgtcggg tttcgccacc 3960
tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta tggaaaaacg 4020
ccagcaacgc ggcctttta cggttcctgg ccttttgctg gccttttgct cacatgttct 4080
ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag tgagctgata 4140
ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa gcggaagagc 4200
gcccaatacg caaaccgcct ctccccgcgc gttggccgat tcattaatgc agaattaatt 4260
ctcatgtttg acagcttatc atcgactgca cggtgcacca atgcttctgg cgtcaggcag 4320
ccatcggaag ctgtggtatg gctgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc 4380
aaggcgcact cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa 4440
tattctgaaa tgagctgttg acaattaatc atcggctcgt ataatgtgtg gaattgtgag 4500
cggataacaa tttcacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg 4560
tggcccgagt gctgcagagg ctgtgcgagc gcggcgcgaa gaacgtgctg gccttcggct 4620
tcgcgctgct ggacggggcc cgcgggggcc cccccgaggc cttcaccacc agcgtgcgca 4680
gctacctgcc caacacggtg accgacgcac tgcgggggag cggggcgtgg gggctgctgc 4740
tgcgccgcgt gggcgacgac gtgctggttc acctgctggc acgctgcgcg ctctttgtgc 4800
tggtggctcc cagctgcgcc taccaggtgt gcgggccgcc gctgtaccag ctcggcgctg 4860
ccactcaggc ccggcccccg ccacacgcta gtggaccccg aaggcgtctg ggatgcgaac 4920
gggcctggaa ccatagcgtc agggaggccg gggtccccct gggcctgcca gccccgggtg 4980
cgaggaggcg cgggggcagt gccagccgaa gtctgccgtt gcccaagagg cccaggcgtg 5040
gcgctgcccc tgagccggag cggacgcccg ttgggcaggg gtcctgggcc cacccgggca 5100
ggacgcgtgg accgagtgac cgtggtttct gtgtggtgtc acctgccaga cccgccgaag 5160
aagccacctc tttggagggt gcgctctctg gcacgcgcca ctcccaccca tccgtgggcc 5220
gccagcacca cgcgggcccc ccatccacat cgcggccacc acgtccctgg gacacgcctt 5280
gtcccccggt gtacgccgag accaagcact tcctctactc ctcaggcgac aaggagcagc 5340
tgcggccctc cttcctactc agctctctga ggcccagcct gactggcgct cggaggctcg 5400
tggagaccat ctttctgggt tccaggccct ggatgccagg gactccccgc aggttgcccc 5460
gcctgcccca gcgctactgg caaatgcggc ccctgtttct ggagctgctt gggaaccacg 5520
cgcagtgccc ctacggggtg ctcctcaaga cgcactgccc gctgcgagct gcggtcaccc 5580
cagcagccgg tgtctgtgcc cgggagaagc cccagggctc tgtggcggcc cccgaggagg 5640
aggacacaga cccccgtcgc ctggtgcagc tgctccgcca gcacagcagc ccctggcagg 5700
tgtacggctt cgtgcgggcc tgcctgcgcc ggctggtgcc cccaggcctc tggggctcca 5760
ggcacaacga acgccgcttc ctcaggaaca ccaagaagtt catctccctg gggaagcatg 5820
ccaagctctc gctgcaggag ctgacgtgga agatgagcgt gcgggactgc gcttggctgc 5880
gcaggagccc aggggttggc tgtgttccgg ccgcagagca ccgtctgcgt gaggagatcc 5940
tggccaagtt cctgcactgg ctgatgagtg tgtacgtcgt cgagctgctc aggtctttct 6000
tttatgtcac ggagaccacg tttcaaaaga acaggctctt tttctaccgg aagagtgtct 6060
ggagcaagtt gcaaagcatt ggaatcagac agcacttgaa gagggtgcag ctgcgggagc 6120
tgtcggaagc agaggtcagg cagcatcggg aagccaggcc cgccctgctg acgtccagac 6180
tccgcttcat ccccaagcct gacgggctgc ggccgattgt gaacatggac tacgtcgtgg 6240
gagccagaac gttccgcaga gaaaagaggg ccgagcgtct cacctcgagg gtgaaggcac 6300
tgttcagcgt gctcaactac gagcgggcgc ggcgccccgg cctcctgggc gcctctgtgc 6360
tgggcctgga cgatatccac agggcctggc gcaccttcgt gctgcgtgtg cgggcccagg 6420
acccgccgcc tgagctgtac tttgtcaagg acaggctcac ggaggtcatc gccagcatca 6480
tcaaacccag aacacgtact gcgtgcgtcg gtatgccgtg gtccagaagg ccgcccatgg 6540
gcacgtccgc aaggccttca agagccacgt ctctaccttg acagacctcc agccgtacat 6600

D10

gcgacagttc gtggctcacc tgcaggagac cagcccgctg agggatgccg tcgtcatcga 6660
gcagagctcc tccctgaatg aggccagcag tggcctcttc gacgtcttcc tacgcttcat 6720
gtgccaccac gccgtgcgca tcaggggcaa gtcctacgtc cagtgccagg ggatcccgca 6780
gggctccatc ctctccacgc tgctctgcag cctgtgctac ggcgacatgg agaacaagct 6840
gtttgcgggg attcggcggg acgggctgct cctgcgtttg gtggatgatt tcttgttggt 6900
gacacctcac ctcacccacg cgaaaacctt cctcaggacc ctggtccgag gtgtccctga 6960
gtatggctgc gtggtgaact tgcggaagac agtggtgaac ttccctgtag aagacgaggc 7020
cctgggtggc acggcttttg ttcagatgcc ggcccacggc ctattccccc ggtgcggcct 7080
gctgctggat acccggaccc tggaggtgca gagcgactac tccagctatg cccggacctc 7140
catcagagcc agtctcacct tcaaccgcgg cttcaaggct gggaggaaca tgcgtcgcaa 7200
actctttggg gtcttgcggc tgaagtgtca cagcctgttt ctggatttgc aggtgaacag 7260
cctccagacg gtgtgcacca acatctacaa gatcctcctg ctgcaggcgt acaggtttca 7320
cgcatgtgtg ctgcagctcc catttcatca gcaagtttgg aagaacccca cattttcct 7380
gcgcgtcatc tctgacacgg cctccctctg ctactccatc ctgaaagcca agaacgcagg 7440
gatgtcgctg ggggccaagg gcgccgccgg ccctctgccc tccgaggccg tgcagtggct 7500
gtgccaccaa gcattcctgc tcaagctgac tcgacaccgt gtcacctacg tgccactcct 7560
ggggtcactc aggacagccc agacgcagct gagtcggaag ctcccgggga cgacgctgac 7620
tgccctggag gccgcagcca acccggcact gccctcagac ttcaagacca tcctggactg 7680
atctagag 7688

<210> 90
<211> 8
<212> PRT
<213> Homo sapiens

<400> 90
Ala Val Arg Ile Arg Gly Lys Ser
1 5

D10

<210> 91
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Consensus P-loop Motif Sequence found in large number of protein families

<220>
<221> MOD_RES
<222> (2)..(5)
<223> Wherein Xaa is any residue

<400> 91
Ala Xaa Xaa Xaa Xaa Gly Lys Ser
1 5

<210> 92
<211> 17
<212> PRT
<213> Homo sapiens

<400> 92
Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Cys Val
1 5 10 15

Gly

<210> 93
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Consensus c-Alb SH3 binding peptide

<220>
<221> MOD_RES
<222> (2)..(5)
<223> Wherein Xaa is any residue

<220>
<221> MOD_RES
<222> (7)..(8)
<223> Wherein Xaa is any residue

<400> 93
Pro Xaa Xaa Xaa Xaa Pro Xaa Xaa Pro
1 5

D10

<210> 94
<211> 17
<212> PRT
<213> Homo sapiens

<400> 94
His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr
1 5 10 15

Pro

<210> 95
<211> 14
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism: General Target Sequence Recognized by Hairpin Ribozyme

<220>
<221> modified_base
<222> (1)..(3)
<223> Wherein N is G, U, C or A

<220>
<221> modified_base

<222> (5)
<223> Wherein N is G, U, C or A

<220>
<221> modified_base
<222> (9)..(14)
<223> Wherein N is G, U, C or A

<400> 95
nnnbngucnn nnnn 14

<210> 96
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

<400> 96
aggagatctc gcgatgccgc gcgctc 26

<210> 97
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

D10

<400> 97
tccacgcgtc ctgcccgggt g 21

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

<400> 98
gctggtgcag cgcggggacc 20

<210> 99
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank

Accession Number AA281296

<400> 99
cacaagcttg aattcacatc tcaccatgaa ggagctggtg gcccgagt 48

<210> 100
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 100
ggcacgcaca ccaggcactg 20

<210> 101
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 101
cctgcctgaa ggagctggtg 20

D10

<210> 102
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 102
ggacacctgg cggaaggag 19

<210> 103
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 103
ccgagtgctg cagaggctgt 20

<210> 104

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 104
gaagccgaag gccagcacgt tctt 24

<210> 105
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 105
gtgcagctgc tccgccagca ca 22

<210> 106
<211> 24
<212> DNA
D10 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 106
gttcccaagc agctccagaa acag 24

<210> 107
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 107
ggcagtgcgt cttgaggagc a 21

<210> 108
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized

Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 108
cactggctga tgagtgtgta c 21

<210> 109
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 109
gacgtacaca ctcatcagcc ag 22

<210> 110
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

D10 <400> 110
ggtctttctt ttatgtcacg gag 23

<210> 111
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 111
cacttgaaga gggtgcagct 20

<210> 112
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 112
gtctcacctc gagggtgaag 20

<210> 113
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 113
ttcaccctcg aggtgagacg ct 22

<210> 114
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 114
tcgtagttga gcacgctgaa c 21

<210> 115
<211> 21
<212> DNA
D10 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 115
gcctgagctg tactttgtca a 21

<210> 116
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 116
ctgagctgta ctttgtcaag gaca 24

<210> 117
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 117
gtacatgcga cagttcgtgg ctca 24

<210> 118
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 118
catgaagcgt aggaagacgt cgaaga 26

<210> 119
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

D10

<400> 119
cgcaaacagc ttgttctcca tgtc 24

<210> 120
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 120
ctatgcccgg acctccatca ga 22

<210> 121
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 121
ctgatggagg tccgggcata g 21

<210> 122
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 122
cctccgaggc cgtgcagt 18

<210> 123
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 123
cacctcaagc tttctagatc agtccaggat ggtcttgaag tca 43

D10

<210> 124
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 124
ggaaggcaaa ggagggcagg gcga 24

<210> 125
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 125
cacgaattcg gatccaagct ttttttttt ttttttt 37

<210> 126
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 126
gggttgcgga gggtgggc 18

<210> 127
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 127
gcagtggtga gccgagtcct g 21

<210> 128
<211> 20
<212> DNA
<213> Artificial Sequence

D10
<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 128
cgactttgga ggtgccttca 20

<210> 129
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 129
gctggtgcag cgcggggacc 20

<210> 130
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 130

gaggtgcaga gcgactactc ca 22

<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 131
gtctcacctc gagggtgaag 20

<210> 132
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 132
ggctgctcct gcgtttggtg ga 22

D10

<210> 133
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 133
gccagagatg gagccaccc 19

<210> 134
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 134
gggtggctcc atctctggc 19

<210> 135
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 135
ccgcacgctc atcttccacg t 21

<210> 136
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 136
gcttggggat gaagcggtc 19

<210> 137
<211> 21
<212> DNA
<213> Artificial Sequence

D10
<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 137
cgcctgagct gtactttgtc a 21

<210> 138
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 138
cacctcaagc tttctagatc agctagcggc ccagcccaac tcccct 46

<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 139
gcagcacaca tgcgtgaaac ctgt 24

<210> 140
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 140
gtgtcagaga tgacgcgcag gaa 23

<210> 141
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

D10 <400> 141
acccacactt gcctgtcctg agt 23

<210> 142
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 142
actggatcct tgacaattaa tgcatcggct cgtataatgt gtggagggtt gcggagggtg 60
ggc 63

<210> 143
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 143
ctgtaatacg actcactata gggttgcgga gggtgggc 38

<210> 144
<211> 73

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 144
cacctgcaga catgcgtttc gtcctcacgg actcatcagg ccagctggcg acgcatgtgt 60
gagccgagtc ctg 73

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 145
ggatccgccg cagagcaccg tctg 24

D10

<210> 146
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 146
cgaagctttc agtgggccgg catctgaac 29

<210> 147
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 147
cgaagctttc acaggcccag cccaactcc 29

<210> 148
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized

Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 148
gcggatccag agccacgtcc tacgtc 26

<210> 149
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 149
gcggatccgt tcagatgccg gcccac 26

<210> 150
<211> 9
<212> PRT
<213> Homo sapiens

<400> 150
Pro Glu Met Glu Pro Pro Arg Arg Pro
1 5

D10

<210> 151
<211> 4
<212> PRT
<213> Homo sapiens

<400> 151
Ala Ala Glu His
1

<210> 152
<211> 6
<212> PRT
<213> Homo sapiens

<400> 152
Val Gln Met Pro Ala His
1 5

<210> 153
<211> 5
<212> PRT
<213> Homo sapiens

<400> 153
Val Gly Leu Gly Leu
1 5

<210> 154
<211> 4
<212> PRT
<213> Homo sapiens

<400> 154
Arg Ala Thr Ser
1

<210> 155
<211> 622
<212> PRT
<213> Homo sapiens

<220>
<223> N-Terminal Truncated Telomerase (ver.2); encoded by SEQ ID NO:51, with Y Intron ORF3

<400> 155
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

```
        195                 200                 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
    210                 215                 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225                 230                 235                 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                 250                 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
            260                 265                 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
        275                 280                 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
    290                 295                 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305                 310                 315                 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
                325                 330                 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
            340                 345                 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
        355                 360                 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
    370                 375                 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385                 390                 395                 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
                405                 410                 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
            420                 425                 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
        435                 440                 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
    450                 455                 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465                 470                 475                 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                 490                 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
            500                 505                 510
```

D10

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

DIO Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
610 615 620